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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:25:42 ; Search time 9.25 Seconds  
(without alignments)  
101.679 Million cell updates/sec

Title: US-10-087-464-1  
Perfect score: 104  
Sequence: 1 GMPWLSATTVRSTHANALT 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	911	1 B3AT_HUMAN	P02730 homo sapien
2	104	100.0	927	1 B3AT_RAT	P23562 rattus norv
3	104	100.0	929	1 B3AT_MOUSE	P04919 mus musculus
4	100	96.2	922	1 B3AT_CHICK	P15575 gallus gall
5	95	91.3	918	1 B3AT_ONCMY	P32847 oncorhynch
6	93	89.4	1234	1 B3A2_RAT	P23347 rattus norv
7	93	89.4	1237	1 B3A2_MOUSE	P13808 mus musculus
8	93	89.4	1237	1 B3A2_RABIT	P48746 oryctolagus
9	93	89.4	1241	1 B3A2_HUMAN	P04920 homo sapien
10	89	85.6	1227	1 B3A3_MOUSE	P16283 mus musculus
11	89	85.6	1227	1 B3A3_RAT	P23348 rattus norv
12	89	85.6	1232	1 B3A3_HUMAN	P48751 homo sapien
13	89	85.6	1233	1 B3A3_RABIT	O18917 oryctolagus
14	83	79.8	1238	1 B3A2_CAVPO	Q32058 cavia porce
15	49	47.1	955	1 B3A4_RABIT	Q99kyl oryctolagus
16	48	46.2	314	1 LIPA_MYCLE	O32962 mycobacteri
17	48	46.2	953	1 B3A4_RAT	Q8k4v2 rattus norv
18	48	46.2	983	1 B3A4_HUMAN	Q96q91 homo sapien
19	45	43.3	302	1 COBK_METH	O27083 methanobact
20	45	43.3	727	1 KDGA_RAT	P51556 rattus norv
21	45	43.3	730	1 KDGA_MOUSE	O88673 mus musculus
22	44	42.3	449	1 C13A_MYCTU	O08447 mycobacteri
23	44	42.3	891	1 SL11_HUMAN	Q95708 hylobates l
24	43	41.3	115	1 NU3M_HYLLA	Q10380 mycobacteri
25	43	41.3	311	1 LIPA_MYCTU	P00749 homo sapien
26	43	41.3	431	1 UROK_HUMAN	Q9c104 schizosacch
27	43	41.3	1076	1 YKT5_SCHPO	P32710 escherichia
28	42.5	40.9	552	1 NRFE_ECOLI	P14176 escherichia
29	42	40.4	354	1 PROW_ECOLI	P41176 escherichia
30	42	40.4	405	1 CYB_RHORI	P23134 rhodospiril
31	42	40.4	827	1 KDGL_CAEEL	Q03603 caenorhabdi
32	41	39.4	322	1 HEM3_CAUCR	Q9ab28 caulobacter
33	41	39.4	442	1 UROK_PIG	P04185 sus scrofa

34 41 39.4 709 1 VM2\_REOVD  
35 41 39.4 734 1 KDGA\_PIG  
36 41 39.4 1092 1 LIFR\_MOUSE  
37 41 39.4 2175 1 POLG\_BOVEV  
38 41 39.4 3301 1 CLR3\_MOUSE  
39 41 39.4 3312 1 CLR3\_HUMAN  
40 41 39.4 3313 1 CLR3\_RAT  
41 40.5 38.9 683 1 SC31\_RAT  
42 40 38.5 263 1 YC56\_PORPU  
43 40 38.5 284 1 COXX\_RHOSH  
44 40 38.5 499 1 CBP1\_HORVU  
45 40 38.5 557 1 HLYB\_SERMA

P11078 reovirus (t  
P20192 sus scrofa  
P42703 mus musculu  
P12915 b genome po  
Q91210 mus musculu  
O9nqv7 homo sapien  
O88278 rattus norv  
Q64319 rattus norv  
P51208 porphyra pu  
P56938 rhodobacter  
P07519 hordeum vul  
P15321 serrattia ma

## ALIGNMENTS

RESULT 1  
B3AT\_HUMAN  
ID B3AT\_HUMAN STANDARD; PRT; 911 AA.  
AC P02730;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)  
DE (CD233 antigen).  
DE SLC4A1 OR AE1 OR EPB3 OR DI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90083213; PubMed=2594752;  
RA Lux S.E., John K.M., Kopito R.R., Lodish H.F.;  
RT "Cloning and characterization of band 3, the human erythrocyte anion-exchange protein (AE1).";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=89134172; PubMed=3223947;  
RA Tanner M.J.A., Martin P.G., High S.;  
RT "The complete amino acid sequence of the human erythrocyte membrane anion-transport protein deduced from the cDNA sequence.";  
RL Biochem. J. 256:703-712(1988).  
RN [3]  
RP SEQUENCE OF 1-199; 220-292 AND 347-370.  
RX MEDLINE=90001294; PubMed=2790053;  
RA Yannoukakos D., Vasseur C., Blouquit Y., Bursaux E., Wajzman H.;  
RT "Primary structure of the cytoplasmic domain of human erythrocyte protein band 3. Comparison with its sequence in the mouse.";  
RL Biochim. Biophys. Acta 998:43-49(1989).  
RN [4]  
RP SEQUENCE OF 1-201.  
RX MEDLINE=83238395; PubMed=6345535;  
RA Kaul R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;  
RT "Amino acid sequence of the N alpha-terminal 201 residues of human erythrocyte membrane band 3.";  
RL J. Biol. Chem. 258:7981-7990(1983).  
RN [5]  
RP SEQUENCE OF 1-3.  
RX MEDLINE=79027186; PubMed=701248;  
RA Drickamer L.K.;  
RT "Orientation of the band 3 polypeptide from human erythrocyte membranes. Identification of NH2-terminal sequence and site of carbohydrate attachment.";  
RL J. Biol. Chem. 253:7242-7248(1978).  
RN [6]  
RP SEQUENCE OF 559-630.  
RX MEDLINE=83308584; PubMed=6615451;  
RA Brock C.J., Tanner M.J.A., Kempf C.;  
RT "The human erythrocyte anion-transport protein. Partial amino acid

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sequence, conformation and a possible molecular mechanism for anion exchange.";  
 RT Biochem. J. 213:577-586(1983).  
 RL [7]  
 RN  
 RP SEQUENCE OF 834-911.  
 RX MEDLINE-88228050; PubMed-3372523;  
 RA Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.;  
 RT "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein.";  
 RL J. Biol. Chem. 263:8232-8238(1988).  
 RN [8]  
 RN  
 RP ROLE OF GLU-681, AND SEQUENCE OF 665-688.  
 RX MEDLINE-92332495; PubMed-1352774;  
 RA Jennings M.L., Smith J.S.;  
 RT "Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681.";  
 RL J. Biol. Chem. 267:13964-13971(1992).  
 RN [9]  
 RN  
 RP PALMITOYLATION OF CYS-843.  
 RX MEDLINE-91358422; PubMed-1885574;  
 RA Okubo K., Hamasaki N., Hara K., Kageura M.;  
 RT "Palmitoylation of cysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLAVAL found in band 3 protein and G2 protein of Rift Valley fever virus.";  
 RL J. Biol. Chem. 266:16420-16424(1991).  
 RN [10]  
 RN  
 RP PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.  
 RX MEDLINE-20400020; PubMed-10942405;  
 RA Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E.,  
 RA Pinna L.A., Donella-Deana A.;  
 RT "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: Identification of primary and secondary phosphorylation sites.";  
 RL Blood 96:1550-1557(2000).  
 RN [11]  
 RN  
 RP VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-91329825; PubMed-1678289;  
 RA Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J.,  
 RA Wajzman H., Bursaux E.;  
 RT "Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the structural modification (Lys 56-->Glu) by protein chemistry methods.";  
 RL Blood 78:1117-1120(1991).  
 RN [12]  
 RN  
 RP VARIANT HE 400-ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-9210782; PubMed-1722314;  
 RA Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,  
 RA Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;  
 RT "Deletion in erythrocyte band 3 gene in malaria-resistant Southeast Asian ovalocytosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).  
 RN [13]  
 RN  
 RP VARIANT HS ARG-327.  
 RX MEDLINE-92329950; PubMed-1378323;  
 RA Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,  
 RA Cohen C.M.;  
 RT "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2.";  
 RL Blood 80:523-529(1992).  
 RN [14]  
 RN  
 RP VARIANT HE 400-ALA-408 DEL.  
 RX MEDLINE-92167271; PubMed-1539405;  
 RA Schofield A.E., Tanner M.J.A., FINDER J.C., Clough B., Bayley P.M.,  
 RA Nash G.B., Dluzevski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,  
 RA Gratzel W.B.;  
 RT "Basis of unique red cell membrane properties in hereditary ovalocytosis.";  
 RL J. Mol. Biol. 223:949-958(1992).  
 RN [15]  
 RN  
 RP VARIANT HS LEU-868.  
 RX MEDLINE-93343855; PubMed-8343110;

Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;  
 RT "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3.";  
 RL Biochem. J. 293:317-320(1993).  
 RN [16]  
 RN  
 RP VARIANT MONTEFIORE LYS-40.  
 RX MEDLINE-93229758; PubMed-8471774;  
 RA Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,  
 RA Schwartz R.S.;  
 RT "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore).";  
 RL Blood 81:2155-2165(1993).  
 RN [17]  
 RN  
 RP VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.  
 RX MEDLINE-94266802; PubMed-8206915;  
 RA Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;  
 RT "Band 3 Memphis variant II. Altered stilbene disulfonate binding and the Diego (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation Pro-854-->Leu.";  
 RL J. Biol. Chem. 269:16155-16158(1994).  
 RN [18]  
 RN  
 RP VARIANT BLOOD GROUP WR(A).  
 RX MEDLINE-95111140; PubMed-7812009;  
 RA Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,  
 RA Tanner M.J.;  
 RT "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain conditions.";  
 RL Blood 85:541-547(1995).  
 RN [19]  
 RN  
 RP VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.  
 RX MEDLINE-95134893; PubMed-7530501;  
 RA Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,  
 RA Alper S.L., Brugnara C., Wichterle H., Palek J.;  
 RT "Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis.";  
 RL Blood 85:634-640(1995).  
 RN [20]  
 RN  
 RP VARIANT HS ASP-771.  
 RX MEDLINE-96136073; PubMed-8547122;  
 RA Maillet P., Vallier A., Reinhardt W.H., Wyss E.J., Ott P., Texler P.,  
 RA Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;  
 RT "Band 3 Chur, a variant associated with band 3-deficient hereditary spherocytosis and substitution in a highly conserved position of transmembrane segment 11.";  
 RL Br. J. Haematol. 91:804-810(1995).  
 RN [21]  
 RN  
 RP VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.  
 RX MEDLINE-97099297; PubMed-8943874;  
 RA Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T.,  
 RA Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,  
 RA Palek J.;  
 RT "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency.";  
 RL Blood 88:4366-4374(1996).  
 RN [22]  
 RN  
 RP VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.  
 RX MEDLINE-96225450; PubMed-8640229;  
 RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,  
 RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,  
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";  
 RL Nat. Genet. 13:214-218(1996).  
 RN [23]  
 RN  
 RP VARIANTS HS SER-147 AND MET-488.  
 RX MEDLINE-97351102; PubMed-9207478;  
 RA Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon M.,  
 RA Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,

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Query Match 100.0%; Score 104; DB 1; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
 DB 720 GMPWLSATTVRSVTHANALT 739  
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RESULT 2  
 B3AT\_RAT STANDARD; PRT; 927 AA.  
 AC P23562;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1).  
 GN SLC4A1 OR AEL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 46-927 FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=89255254; PubMed=2722777;  
 RA Kudrycki K.E., Shull G.E.;  
 RT "Primary structure of the rat kidney band 3 anion exchange protein deduced from a cDNA."  
 RL J. Biol. Chem. 264:8185-8192(1989).  
 RN [2]  
 RP SEQUENCE OF 1-45 FROM N.A.  
 RA Kudrycki K.E., Shull G.E.;  
 RL Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).  
 CC -1- SUBUNIT: A DIMER IN SOLUTION. IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND COLLECTING DUCTS.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Erythrocyte;  
 CC IsoId=P23562-1; Sequence=Displayed;  
 CC Name=Kidney;  
 CC IsoId=P23562-2; Sequence=VSP\_000455;  
 CC -1- TISSUE SPECIFICITY: Kidney.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; J04793; AAA0800.1; ALP\_INIT.  
 CC EMBL; L02943; AAA40801.1; -.  
 CC PIR; A33810; A33810.  
 CC HSP; P02730; IRTS.  
 CC InterPro; IPR001717; Anion\_exchange.  
 CC InterPro; IPR003020; HCO3\_cotransp.  
 CC Pfam; PF00955; HCO3\_cotransp; 1.  
 CC PRINTS; PR01231; HCO3TRNSPORT.  
 CC TIGRFAMs; TIGR00834; ae; 1.  
 CC PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 CC PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 CC Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;

Lipoprotein; Palmitate; Alternative splicing.  
 KW DOMAIN 1 420 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 421 927 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 441 441 POTENTIAL.  
 FT TRANSMEM 454 473 POTENTIAL.  
 FT TRANSMEM 477 496 POTENTIAL.  
 FT TRANSMEM 508 527 POTENTIAL.  
 FT TRANSMEM 540 558 POTENTIAL.  
 FT TRANSMEM 559 585 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 585 604 POTENTIAL.  
 FT TRANSMEM 605 619 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 620 640 POTENTIAL.  
 FT TRANSMEM 641 676 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 677 696 POTENTIAL.  
 FT TRANSMEM 715 735 POTENTIAL.  
 FT TRANSMEM 779 796 POTENTIAL.  
 FT TRANSMEM 801 822 POTENTIAL.  
 FT TRANSMEM 860 881 POTENTIAL.  
 FT CARBOHYD 658 658 N-LINKED (GLCNAC... ) (PROBABLE).  
 FT LIPID 859 859 PALMITATE (BY SIMILARITY).  
 FT VARSPLIC 1 79 Missing (in isoform kidney).  
 FT SEQUENCE 927 AA; 103172 MW; 681A228474E5E9DE CRC64;  
 SQ  
 Query Match 100.0%; Score 104; DB 1; Length 927;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
 DB 736 GMPWLSATTVRSVTHANALT 755  
 |||||||||||||||||||

RESULT 3  
 B3AT\_MOUSE STANDARD; PRT; 929 AA.  
 AC P04919;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1) (MEB3).  
 DE SLC4A1 OR AEL.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85268011; PubMed=2410791;  
 RA Kopito R.R., Lodish H.F.;  
 RT "Primary structure and transmembrane orientation of the murine anion exchange protein."  
 RL Nature 316:234-238(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86034211; PubMed=3840489;  
 RA Kopito R.R., Lodish H.F.;  
 RT "Structure of the murine anion exchange protein."  
 RL J. Cell. Biochem. 29:1-17(1985).  
 RN [3]  
 RP PARTIAL SEQUENCE FROM N.A.  
 RX MEDLINE=87250387; PubMed=3036795;  
 RA Kopito R.R., Andersson M., Lodish H.F.;  
 RT "Structure and organization of the murine band 3 gene."  
 RL J. Biol. Chem. 262:8035-8040(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX Kopito R.R.;  
 RL Submitted (JUL-1987) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 11-929 FROM N.A.  
 RX MEDLINE=86274622; PubMed=3015590;

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RA Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,  
 RA Cioe L., Rovera G., Curtis P.J.;  
 RT "Cloning and structural characterization of a human non-erythroid  
 RT band 3-like protein";  
 RL EMBO J. 5:1205-1214(1986).  
 RN [6]  
 RP SEQUENCE OF 33-47: 360-375; 382-395 AND 578-590.  
 RX MEDLINE-89229233; PubMed-2713407;  
 RA Raiba M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,  
 RA Passow H.;  
 RT "Major proteolytic fragments of the murine band 3 protein as obtained  
 RT after in situ proteolysis";  
 RL Biochim. Biophys. Acta 980:291-298(1989).  
 CC -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE  
 CC ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS  
 CC INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS  
 CC THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING  
 CC SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND  
 CC HEMOGLOBIN.  
 CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 CC AND APPEARS TO BE TETRAMERIC.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Erythrocyte;  
 CC IsoId=P04919-1; Sequence=Displayed;  
 CC Name=Kidney;  
 CC IsoId=P04919-2; Sequence=VSP\_000454;  
 CC -1- TISSUE SPECIFICITY: ERYTHROCYTE.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X02677; CAA26506.1; -;  
 DR EMBL; M29379; AAA37187.1; -;  
 DR EMBL; J02756; AAA37278.1; -;  
 DR EMBL; X03917; CAA27555.1; -;  
 DR PIR; A25314; A25314.  
 DR HSP; P02730; IRTS.  
 DR MGD; MGI-109393; Slc4a1.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR Pfam; PF00955; HCO3\_cotransp.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;  
 KW Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 422 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 423 443 POTENTIAL.  
 FT TRANSMEM 456 475 POTENTIAL.  
 FT TRANSMEM 479 498 POTENTIAL.  
 FT TRANSMEM 510 529 POTENTIAL.  
 FT TRANSMEM 542 560 POTENTIAL.  
 FT DOMAIN 561 586 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 587 606 POTENTIAL.  
 FT DOMAIN 607 621 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 622 642 POTENTIAL.  
 FT DOMAIN 643 678 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 679 698 POTENTIAL.  
 FT TRANSMEM 717 737 POTENTIAL.  
 FT TRANSMEM 781 798 POTENTIAL.  
 FT TRANSMEM 803 824 POTENTIAL.  
 FT TRANSMEM 862 883 POTENTIAL.  
 FT CARBOHYD 660 660 N-LINKED (GLCNAC... ) (PROBABLE).

FT LIPID 861 861 PALMITATE (BY SIMILARITY).  
 FT VARSPLIC 1 79 Missing (in isoform Kidney).  
 FT CONFLICT 467 467 /FTId=VSP\_000454.  
 FT G -> S (IN REF. 5).  
 SQ SEQUENCE 929 AA; 103135 MW; 5C0E281C394FB614 CRC64;  
 Query Match 100.0%; Score 104; DB 1; Length 929;  
 Best Local Similarity 100.0%; Pred.No. 4.4e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GMPWLSATTVRSVTHANALT 20  
 Db 738 GMPWLSATTVRSVTHANALT 757  
 RESULT 4  
 B3AT\_CHICK  
 ID B3AT\_CHICK STANDARD; PRT; 922 AA.  
 AC P15575;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DE 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Band 3 anion transport protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-89039870; PubMed-3185555;  
 RA Kim H.R.C., Yew N.S., Ansorge W., Voss H., Schwager C.,  
 RA Vennstrom B., Zenke M., Engel J.D.;  
 RT "Two different mRNAs are transcribed from a single genomic locus  
 RT encoding the chicken erythrocyte anion transport proteins (band 3).";  
 RL Mol. Cell. Biol. 8:4416-4424(1988).  
 CC -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE  
 CC ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS  
 CC INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS  
 CC THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING  
 CC SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND  
 CC HEMOGLOBIN.  
 CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 CC AND APPEARS TO BE TETRAMERIC.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: ERYTHROCYTE.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M23404; AAA48753.1; -;  
 DR HSP; P02730; IRTQ.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.  
 FT DOMAIN 1 416 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 417 922 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 417 437 POTENTIAL.  
 FT TRANSMEM 450 469 POTENTIAL.  
 FT TRANSMEM 473 492 POTENTIAL.  
 FT TRANSMEM 504 523 POTENTIAL.  
 FT TRANSMEM 536 554 POTENTIAL.

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FT DOMAIN 555 579 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSSEM 580 599 POTENTIAL.
FT DOMAIN 600 614 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 615 635 POTENTIAL.
FT DOMAIN 636 671 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSSEM 672 691 POTENTIAL.
FT TRANSSEM 710 730 POTENTIAL.
FT TRANSSEM 774 791 POTENTIAL.
FT TRANSSEM 796 817 POTENTIAL.
FT TRANSSEM 855 876 POTENTIAL.
FT CARBOHYD 653 653 N-LINKED (GLCNAC... ) (PROBABLE).
SQ SEQUENCE 922 AA; 102223 MW; FF4ECAD6D60CF0CF CRC64;

Query Match 96.2%; Score 100; DB 1; Length 922;
Best Local Similarity 90.0%; Pred. No. 2e-08;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATVRSVTHANALT 20
DB 731 GMPWLSATVRSVTHANALT 750
|||||

RESULT 5
B3AT_ONCMY STANDARD; PRT; 918 AA.
ID B3AT_ONCMY AC P32847;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Band 3 anion exchange protein.
GN SIC4AL OR AEL.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92344566; PubMed=1637296;
RX Hubner S., Michel F., Rudloff V., Appelhans H.;
RT "Amino acid sequence of band-3 protein from rainbow trout
erythrocytes derived from cDNA.";
RL Biochem. J. 285:17-23(1992).
CC -1- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).
CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
AND APPEARS TO BE TETRAMERIC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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EMBL; X61699; CNA43868.1;
PIR; S24318; S24318.
HSP; P02730; IRTQ.
InterPro; IPR001171; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp.1.
DR PRINTS; PR01233; HCO3TRNSPOT.
DR TIGRfams; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Anion exchange; Lipoprotein; Palmitate.
FT DOMAIN 1 392 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 393 918 MEMBRANE (ANION EXCHANGE).

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FT TRANSSEM 393 413 POTENTIAL.
FT TRANSSEM 426 445 POTENTIAL.
FT TRANSSEM 449 468 POTENTIAL.
FT TRANSSEM 480 499 POTENTIAL.
FT TRANSSEM 512 530 POTENTIAL.
FT DOMAIN 531 581 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSSEM 582 601 POTENTIAL.
FT DOMAIN 602 616 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 617 637 POTENTIAL.
FT DOMAIN 638 673 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSSEM 674 693 POTENTIAL.
FT TRANSSEM 712 732 POTENTIAL.
FT TRANSSEM 772 789 POTENTIAL.
FT TRANSSEM 794 815 POTENTIAL.
FT TRANSSEM 853 874 POTENTIAL.
FT LIPID 852 852 PALMITATE (BY SIMILARITY).
FT CARBOHYD 546 546 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 568 568 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 918 AA; 101893 MW; 37E163141FBD16A CRC64;

Query Match 91.3%; Score 95; DB 1; Length 918;
Best Local Similarity 90.0%; Pred. No. 1.3e-07;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATVRSVTHANALT 20
DB 733 GMPWLSATVRSVTHANALT 752
|||||

RESULT 6
B3A2_RAT STANDARD; PRT; 1234 AA.
ID B3A2_RAT AC P23347;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
GN SLC4A2 OR AE2 OR B3RP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Stomach;
RX MEDLINE=90094439; PubMed=2294114;
RA Kudrycki K.E., Newman P.R., Shull G.E.;
RT "cDNA cloning and tissue distribution of mRNAs for two proteins that
are related to the band 3 Cl-/HCO3-exchanger.";
RL J. Biol. Chem. 265:462-471(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90319095; PubMed=2371270;
RX Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
Kopito R.R.;
RT "Functional expression and subcellular localization of an anion
exchanger cloned from choroid plexus.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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EMBL; J05166; AAA40799.1;

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-1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=5;

Name=A;

  IsoId=Pl3808-1; Sequence=Displayed;

Name=B1;

  IsoId=Pl3808-2; Sequence=VSP\_000458;

Name=B2;

  IsoId=Pl3808-3; Sequence=VSP\_000457;

Name=C1;

  IsoId=Pl3808-4; Sequence=VSP\_000460;

Name=C2;

  IsoId=Pl3808-5; Sequence=VSP\_000459, VSP\_000461;

-1- TISSUE SPECIFICITY: Isoform a is widely expressed at similar levels in all tissues examined. Isoforms b1 and b2 are predominantly expressed in stomach although they are also detected at lower levels in other tissues. Isoform c1 is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and stomach than in other tissues.

-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

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EMBL; J04036; AAA65505.1; -

EMBL; AF255774; AAG23154.1; -

EMBL; AF255774; AAG23155.1; -

EMBL; AF255774; AAG23156.1; -

EMBL; AF255774; AAG23157.1; -

EMBL; AF255774; AAG23158.1; -

PIR; A31789; A31789.

HSSP; P02730; 1BTQ.

MGD; MGI:109351; Slc4a2.

InterPro; IPR001717; Anion\_exchange.

InterPro; IPR003020; HCO3\_cotransp.

Pfam; PF00955; HCO3\_cotransp; 1.

PRINTS; PR01231; HCO3TRNSPORT.

TIGRams; TIGR00834; ae; 1.

PROSITE; PS002219; ANION\_EXCHANGER\_1; 1.

PROSITE; PS002220; ANION\_EXCHANGER\_2; 1.

Transmembrane; Glycoprotein; Transp; Antipor; Ion transport; Anion exchange; Lipoprotein; Palmitate; Alternative splicing.

KW ANION\_EXCHNG; 1 703 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 1 703 MEMBRANE (ANION EXCHANGE).

FT TRANSNM 704 1237 POTENTIAL.

FT TRANSNM 704 727 POTENTIAL.

FT TRANSNM 733 770 POTENTIAL.

FT TRANSNM 790 812 POTENTIAL.

FT TRANSNM 822 843 POTENTIAL.

FT DOMAIN 844 896 EXOPLASMIC LOOP (POTENTIAL).

FT TRANSNM 897 914 POTENTIAL.

FT DOMAIN 915 929 CYTOPLASMIC (POTENTIAL).

FT TRANSNM 930 950 POTENTIAL.

FT TRANSNM 984 1006 POTENTIAL.

FT TRANSNM 1032 1053 POTENTIAL.

FT TRANSNM 1087 1132 POTENTIAL.

FT TRANSNM 1159 1195 POTENTIAL.

FT DOMAIN 5 316 PRO-RICH.

FT DOMAIN 73 87 HIS-RICH.

FT DOMAIN 861 865 POLY-SER.

FT CARBOHYD 855 855 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT LIPID 1169 1169 PALMITATE (BY SIMILARITY).

FT VARSPLIC 1 17 MSAAPRRPASGDSLT -> MDFLLRPQ (in isoform B2).

FT -FTId=VSP\_000457.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:25:42 ; Search time 9.25 Seconds  
(without alignments)  
101.679 Million cell updates/sec

Title: US-10-087-464-2

Perfect score: 98

Sequence: 1 SVTHANALTVMGKASTPGAA 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	911	1 B3AT_HUMAN	P02730 homo sapien
2	91	92.9	927	1 B3AT_RAT	P23562 rattus norv
3	91	92.9	929	1 B3AT_MOUSE	P04919 mus musculu
4	73	74.5	1234	1 B3A2_RAT	P23347 rattus norv
5	73	74.5	1237	1 B3A2_MOUSE	P13808 mus musculu
6	73	74.5	1237	1 B3A2_RABIT	P48746 oryctolagus
7	73	74.5	1238	1 B3A2_CAVPO	P02058 cavia porce
8	73	74.5	1241	1 B3A2_HUMAN	P04920 homo sapien
9	71	72.4	922	1 B3AT_CHICK	P15575 gallus gall
10	63	64.3	918	1 B3AT_ONCMY	P32847 oncorhynch
11	61	62.2	1227	1 B3A3_MOUSE	P16283 mus musculu
12	61	62.2	1227	1 B3A3_RAT	P23348 rattus norv
13	61	62.2	1232	1 B3A3_HUMAN	P48751 rattus norv
14	61	62.2	1233	1 B3A3_RABIT	O18917 oryctolagus
15	49	50.0	262	1 Y003_HAEIN	P44447 haemophilus
16	48	49.0	1655	1 OMPB_RICCN	Q9kka3 r outer mem
17	47	48.0	1300	1 120K_RICRI	P14914 rickettsia
18	47	48.0	1654	1 OMPB_RICRI	Q53047 r outer mem
19	42.5	43.4	706	1 NUCPL_HUMAN	P19338 homo sapien
20	42	42.9	303	1 FTSY_RICPR	O05948 rickettsia
21	41.5	42.3	495	1 WD21_HUMAN	Q8wvl6 homo sapien
22	41	41.8	122	1 YFC5_SHEFR	Q02482 shewanella
23	41	41.8	256	1 TPIS_AGRF5	O8uey3 agrobacteri
24	40	40.8	270	1 PANB_OCEIH	O8elf4 oceanobacil
25	40	40.8	312	1 YEIN_ECOLI	P33025 escherichia
26	40	40.8	568	1 PUR6_CANAL	Q92210 candida alb
27	40	40.8	779	1 Y700_MYCTU	Q10821 mycobacteri
28	40	40.8	874	1 BCAL_MOUSE	Q61140 mus musculu
29	40	40.8	968	1 BCAL_RAT	O63767 rattus norv
30	39	39.8	190	1 PEP_PLAFA	P34189 plasmodium
31	39	39.8	399	1 BR53_MOUSE	O34798 mus musculu
32	39	39.8	402	1 ALP_CEPAC	P29118 cephalospor
33	39	39.8	402	1 OPS4_CANAL	P46596 candida alb

34	39	39.8	529	1 YPC1_CAEEL	Q11178 caenorhabdi
35	39	39.8	662	1 MUC1_XENLA	Q05049 xenopus lae
36	39	39.8	681	1 TBRI_MOUSE	Q64336 mus musculu
37	39	39.8	682	1 RTN1_HUMAN	Q16650 homo sapien
38	39	39.8	776	1 RTN1_HUMAN	Q16799 homo sapien
39	38.5	39.3	356	1 EGSA_METAC	Q8tjul methanosarc
40	38.5	39.3	390	1 C3L2_HUMAN	Q15782 homo sapien
41	38.5	39.3	470	1 UL49_HSV6U	P52441 human herpe
42	38	38.8	116	1 B2MG_BRARE	Q04475 brachydanio
43	38	38.8	125	1 RSL3_RICCN	Q929y8 rickettsia
44	38	38.8	125	1 RSL3_RICPR	Q92cs7 rickettsia
45	38	38.8	276	1 YXKO_BACSU	P94368 bacillus su

## ALIGNMENTS

RESULT 1  
B3AT\_HUMAN STANDARD; PRT; 911 AA.  
AC P02730;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)  
DE (CD233 antigen).  
GN SLC4A1 OR AE1 OR EPB3 OR DI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90083213; PubMed=2594752;  
RA Lux S.E., John K.M., Kopito R.R., Lodish H.F.;  
RT "Cloning and characterization of band 3, the human erythrocyte anion-  
exchange protein (AE1).";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=89134172; PubMed=3223947;  
RA Tanner M.J.A., Martin P.G., High S.;  
RT "The complete amino acid sequence of the human erythrocyte membrane  
anion-transport protein deduced from the cDNA sequence.";  
RL Biochem. J. 256:703-712(1988).  
RN [3]  
RP SEQUENCE OF 1-199; 220-292 AND 347-370.  
RX MEDLINE=90001294; PubMed=2750053;  
RA Yannoukakis D., Vasseur C., Blouquit Y., Bursaux E., Wajzman H.;  
RT "Primary structure of the cytoplasmic domain of human erythrocyte  
protein band 3. Comparison with its sequence in the mouse.";  
RL Biochim. Biophys. Acta 998:43-49(1989).  
RN [4]  
RP SEQUENCE OF 1-201.  
RX MEDLINE=83238395; PubMed=6345535;  
RA Kaul R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;  
RT "Amino acid sequence of the N alpha-terminal 201 residues of human  
erythrocyte membrane band 3.";  
RL J. Biol. Chem. 258:7981-7990(1983).  
RN [5]  
RP SEQUENCE OF 1-3.  
RX MEDLINE=79027186; PubMed=701248;  
RA Drickamer L.K.;  
RT "Orientation of the band 3 polypeptide from human erythrocyte  
membranes. Identification of NH2-terminal sequence and site of  
carbohydrate attachment.";  
RL J. Biol. Chem. 253:7242-7248(1978).  
RN [6]  
RP SEQUENCE OF 559-630.  
RX MEDLINE=83308584; PubMed=6615451;  
RA Brock C.J., Tanner M.J.A., Kempf C.;  
RT "The human erythrocyte anion-transport protein. Partial amino acid

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RT sequence, conformation and a possible molecular mechanism for anion  
 RT exchange.";  
 RL Biochem. J. 213:577-586(1983).  
 RN [7]  
 RP MEDLINE-82228050; PubMed-3372523;  
 RX MEDLINE-91358422; PubMed-1885574;  
 RA Okubo K., Hamasaki N., Hara K., Kageura M.;  
 RT "Palmitoylation of cysteine 69 from the COOH-terminal of band 3  
 RT protein in the human erythrocyte membrane. Acylation occurs in the  
 RT middle of the consensus sequence of F-I-IICLAVL found in band 3  
 RT protein and G2 protein of Rift Valley fever virus.";  
 RL J. Biol. Chem. 266:16420-16424(1991).  
 RN [10]  
 RP PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.  
 RX MEDLINE-20400020; PubMed-10942405;  
 RA Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E.,  
 RA Pinna L.A., Donella-Deana A.;  
 RT "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine  
 RT kinases in intact human erythrocytes: identification of primary and  
 RT secondary phosphorylation sites.";  
 RL Blood 96:1550-1557(2000).  
 RN [11]  
 RP VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-91329825; PubMed-1678289;  
 RA Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J.,  
 RA Wajcman H., Bursaux E.;  
 RT "Human erythrocyte band 3 polymorphism (band 3 Memphis):  
 RT characterization of the structural modification (Lys 56-->Glu) by  
 RT protein chemistry methods.";  
 RL Blood 78:1117-1120(1991).  
 RN [12]  
 RP VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-92107882; PubMed-1722314;  
 RA Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,  
 RA Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;  
 RT "Deletion in erythrocyte band 3 gene in malaria-resistant Southeast  
 RT Asian ovalocytosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).  
 RN [13]  
 RP VARIANT HS ARG-327.  
 RX MEDLINE-92329950; PubMed-1378323;  
 RA Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,  
 RA Cohen C.M.;  
 RT "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic  
 RT domain of erythrocyte band 3 protein associated with spherocytic  
 RT hemolytic anemia and partial deficiency of protein 4.2.";  
 RL Blood 80:523-529(1992).  
 RN [14]  
 RP VARIANT HE 400-ALA--ALA-408 DEL.  
 RX MEDLINE-92167271; PubMed-1538405;  
 RA Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,  
 RA Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,  
 RA Gratzner W.B.;  
 RT "Basis of unique red cell membrane properties in hereditary  
 RT ovalocytosis.";  
 RL J. Mol. Biol. 223:949-958(1992).  
 RN [15]  
 RP VARIANT HS LEU-868.  
 RX MEDLINE-93343855; PubMed-8343110;  
 RA Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,  
 RA Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;  
 RT "Band 3 HT, a human red-cell variant associated with acanthocytosis  
 RT and increased anion transport, carries the mutation Pro-868-->Leu in  
 RL the membrane domain of band 3.";  
 RL Biochem. J. 293:317-320(1993).  
 RN [16]  
 RP VARIANT MONTEFIORE LYS-40.  
 RX MEDLINE-93229758; PubMed-8471774;  
 RA Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,  
 RA Schwartz R.S.;  
 RT "Human erythrocyte protein 4.2 deficiency associated with hemolytic  
 RT anemia and a homozygous 40 glutamic acid-->lysine substitution in the  
 RL cytoplasmic domain of band 3 (band 3Montefiore).";  
 RL Blood 81:2155-2165(1993).  
 RN [17]  
 RP VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.  
 RX MEDLINE-94266802; PubMed-8206915;  
 RA Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;  
 RT "Band 3 Memphis variant II. Altered stilbene disulfonate binding and  
 RT the Diego (Dia) blood group antigen are associated with the human  
 RT erythrocyte band 3 mutation Pro-854-->Leu.";  
 RL J. Biol. Chem. 269:16155-16158(1994).  
 RN [18]  
 RP VARIANT BLOOD GROUP WR(A).  
 RX MEDLINE-95111140; PubMed-7812009;  
 RA Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,  
 RA Tanner M.J.;  
 RT "Changes in the blood group Wright antigens are associated with a  
 RT mutation at amino acid 658 in human erythrocyte band 3: a site of  
 RT interaction between band 3 and glycophorin A under certain  
 RT conditions.";  
 RL Blood 85:541-547(1995).  
 RN [19]  
 RP VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.  
 RX MEDLINE-95134893; PubMed-7530501;  
 RA Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,  
 RA Alper S.L., Brugnara C., Wichterle H., Palek J.;  
 RT "Mutations of conserved arginines in the membrane domain of erythroid  
 RT band 3 lead to a decrease in membrane-associated band 3 and to the  
 RT phenotype of hereditary spherocytosis.";  
 RL Blood 85:634-640(1995).  
 RN [20]  
 RP VARIANT HS ASP-771.  
 RX MEDLINE-96136073; PubMed-8547122;  
 RA Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,  
 RA Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;  
 RT "Band 3 Chur: a variant associated with band 3-deficient hereditary  
 RT spherocytosis and substitution in a highly conserved position of  
 RT transmembrane segment 11.";  
 RL Br. J. Haematol. 91:804-810(1995).  
 RN [21]  
 RP VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.  
 RX MEDLINE-97099297; PubMed-8943874;  
 RA Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T.,  
 RA Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,  
 RA Palek J.;  
 RT "Characterization of 13 novel band 3 gene defects in hereditary  
 RT spherocytosis with band 3 deficiency.";  
 RL Blood 88:4366-4374(1996).  
 RN [22]  
 RP VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.  
 RX MEDLINE-96225450; PubMed-8640229;  
 RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,  
 RA Dornwell M., Herbers J., Kugler W., Ozcan R., Pekrun A.,  
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive  
 RT hereditary spherocytosis.";  
 RL Nat. Genet. 13:214-218(1996).  
 RN [23]  
 RP VARIANTS HS SER-147 AND MET-488.  
 RX MEDLINE-97351102; PubMed-9207478;  
 RA Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon M.,  
 RA Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,

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Query Match      100.0%; Score 98; DB 1; Length 911;
Best Local Similarity 100.0%; Pred No. 1.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVTHANALVTMGKASTPGAA 20
Db 731 SVTHANALVTMGKASTPGAA 750

RESULT 2
B3AT_RAT
ID B3AT_MOUSE STANDARD; PRT; 927 AA.
AC P23562;
DT 01-NOV-1991 (Rel. 20, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
GN SLC4A1 OR AEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 46-927 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=89255254; PubMed=2722777;
RA Kudrycki K.E., Shull G.E.;
RT "Primary structure of the rat kidney band 3 anion exchange protein
deduced from a cDNA.";
RL J. Biol. Chem. 264:8185-8192(1989).
RN [2]
RP SEQUENCE OF 1-45 FROM N.A.
RA Kudrycki K.E., Shull G.E.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
CC MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
CC WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
CC CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).
CC -!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
CC AND APPEARS TO BE TETRAMERIC.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
CC BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
CC COLLECTING DUCTS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Erythrocyte;
CC IsoId=P23562-1; Sequence=Displayed;
CC Name=Kidney;
CC IsoId=P23562-2; Sequence=VSP_000455;
CC -!- TISSUE SPECIFICITY: Kidney.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04793; AAA40800.1; ALT_INIT.
DR EMBL; L02943; AAA40801.1;
DR PIR; A33810; A33810.
DR HSP; P02730; IETS.
DR InterPro; IPR001717; Anion_exchanger.
DR InterPro; IPR03020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGR; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;

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KW Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 420 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 421 927 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 421 441 POTENTIAL.
FT TRANSMEM 454 473 POTENTIAL.
FT TRANSMEM 477 496 POTENTIAL.
FT TRANSMEM 508 527 POTENTIAL.
FT TRANSMEM 540 558 POTENTIAL.
FT DOMAIN 559 585 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 585 604 POTENTIAL.
FT DOMAIN 605 619 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 620 640 EXOPLASMIC LOOP (POTENTIAL).
FT DOMAIN 641 676 POTENTIAL.
FT TRANSMEM 677 735 POTENTIAL.
FT TRANSMEM 779 796 POTENTIAL.
FT TRANSMEM 801 822 POTENTIAL.
FT TRANSMEM 860 881 POTENTIAL.
FT CARBOHYD 658 658 N-LINKED (GLCNAC...) (PROBABLE).
FT LIPID 859 859 PALMITATE (BY SIMILARITY).
FT VARSPLIC 1 79 Missing (in isoform Kidney).
FT SEQUENCE 927 AA; 103172 MW; 681A228474E5E9DE CRC64;
SQ SEQUENCE 927 AA; 103172 MW; 681A228474E5E9DE CRC64;

Query Match      92.9%; Score 91; DB 1; Length 927;
Best Local Similarity 95.0%; Pred No. 2.2e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVTHANALVTMGKASTPGAA 20
Db 747 SVTHANALVTMGKASTPGAA 766

RESULT 3
B3AT_MOUSE
ID B3AT_MOUSE STANDARD; PRT; 929 AA.
AC P04919;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
DE (MEB3).
GN SLC4A1 OR AEL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85268011; PubMed=2410791;
RA Kopito R.R., Lodish H.F.;
RT "Primary structure and transmembrane orientation of the murine anion
exchange protein.";
RL Nature 316:234-238(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86034211; PubMed=3840489;
RA Kopito R.R., Lodish H.F.;
RT "Structure of the murine anion exchange protein.";
RL J. Cell. Biochem. 29:1-17(1985).
RN [3]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=87250387; PubMed=3036795;
RA Kopito R.R., Andersson M., Lodish H.F.;
RT "Structure and organization of the murine band 3 gene.";
RL J. Biol. Chem. 262:8035-8040(1987).
RN [4]
RP SEQUENCE FROM N.A.
RA Kopito R.R.;
RL Submitted (JUL-1987) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 11-929 FROM N.A.
RX MEDLINE=86274622; PubMed=3015590;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:25:42 ; Search time 9.25 Seconds  
(without alignments)  
101.679 Million cell updates/sec

Title: US-10-087-464-3

Perfect score: 96

Sequence: 1 GKASTPGAAQIQEVKEQRI 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	911	1 B3AT_HUMAN	P02730 homo sapien
2	89	92.7	927	1 B3AT_RAT	P23562 rattus norv
3	89	92.7	929	1 B3AT_MOUSE	P04919 mus musculus
4	61	63.5	922	1 B3AT_CHICK	P15575 gallus gall
5	58	60.4	1234	1 B3A2_RAT	P23347 rattus norv
6	58	60.4	1237	1 B3A2_MOUSE	P13808 mus musculus
7	58	60.4	1237	1 B3A2_RABIT	P48746 oryctolagus
8	58	60.4	1238	1 B3A2_CAVPO	Q92088 cavia porce
9	58	60.4	1241	1 B3A2_HUMAN	P04920 homo sapien
10	54	56.2	1227	1 B3A3_MOUSE	P16283 mus musculus
11	54	56.2	1227	1 B3A3_RAT	P23348 rattus norv
12	54	56.2	1232	1 B3A3_HUMAN	P48751 homo sapien
13	54	56.2	1233	1 B3A3_RABIT	O18917 oryctolagus
14	45	46.9	391	1 RRPB_MUMPM	P16072 mumps virus
15	45	46.9	391	1 RRPB_MOUSE	P16595 mumps virus
16	44	45.8	459	1 NCBL_MOUSE	Q02819 mus musculus
17	44	45.8	459	1 NCBL_RAT	Q03083 rattus norv
18	44	45.8	461	1 NCBL_HUMAN	Q02818 homo sapien
19	43	44.8	323	1 RLOC_ARATH	P57691 arabidopsis
20	43	44.8	601	1 YDJO_ECOLI	P38055 escherichia
21	43	44.8	601	1 CORO_SCHPO	O13923 schizosacch
22	42	43.8	448	1 YNO6_YEAST	P53890 saccharomyc
23	41	42.7	210	1 CAC2_HAECC	P16252 haemochus
24	41	42.7	219	1 BASP_RAT	Q05175 rattus norv
25	41	42.7	265	1 DH47_ARATH	P31168 arabidopsis
26	41	42.7	583	1 FOJO_DROME	P54360 drosophila
27	41	42.7	650	1 VE1_HPV72	Q81999 human papil
28	41	42.7	826	1 VILL_HUMAN	P09327 homo sapien
29	41	42.7	826	1 VILL_MOUSE	Q02468 mus musculus
30	41	42.7	950	1 IF2_LACLC	Q9x764 lactococcus
31	41	42.7	2116	1 MS2_DICDI	P02799 dictyosteli
32	41	42.7	2418	1 SPCA_HUMAN	P02549 homo sapien
33	40.5	42.2	500	1 PROP_ECOLI	P30848 escherichia

34	40.5	42.2	500	1	PROP_SALTY	P40862 salmonella
35	40.5	42.2	728	1	PKP1_MOUSE	P97350 mus musculus
36	40	41.7	129	1	RL7_ANASP	Q8Y1J5 anabaena sp
37	40	41.7	144	1	HAP3_YEOST	P13434 saccharomyc
38	40	41.7	186	1	RL12_TOBAC	P24929 nicotiana t
39	40	41.7	444	1	BCHN_CHLAU	O9f6x6 chloroflexu
40	40	41.7	448	1	PRSA_ORYSA	P46466 oryza sativ
41	40	41.7	453	1	RADA_CHLPN	Q929c8 chlamydia p
42	40	41.7	463	1	DRNA_PROS9	Q95487 prochloroco
43	40	41.7	518	1	ATPA_MYCPN	Q05029 mycoplasma
44	40	41.7	594	1	CIK1_YEAST	Q01649 saccharomyc
45	40	41.7	594	1	UL93_HCMVA	P16799 human cytom

ALIGNMENTS

RESULT 1  
B3AT\_HUMAN  
ID B3AT\_HUMAN STANDARD; PRT; 911 AA.  
AC P02730;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)  
DE (CD233 antigen).  
GN SLC4A1 OR AE1 OR EPB3 OR DI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90083213; PubMed=2594752;  
RA Lux S.E., John K.M., Kopito R.R., Lodish H.F.;  
RT "Cloning and characterization of band 3, the human erythrocyte anion-  
exchange protein (AE1).";  
RL proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA MEDLINE=89134172; PubMed=3223947;  
RX Tanner M.J.A., Martin P.G., High S.;  
RT "The complete amino acid sequence of the human erythrocyte membrane  
anion-transport protein deduced from the cDNA sequence.";  
RL Biochem. J. 256:703-712(1988).  
RN [3]  
RP SEQUENCE OF 1-199; 220-292 AND 347-370.  
RX MEDLINE=90001294; PubMed=2790053;  
RA Yannoukakis D., Vasseur C., Blouquit Y., Bursaux E., Wajzman H.;  
RT "Primary structure of the cytoplasmic domain of human erythrocyte  
protein band 3. Comparison with its sequence in the mouse.";  
RL Biochim. Biophys. Acta 998:43-49(1989).  
RN [4]  
RP SEQUENCE OF 1-201.  
RX MEDLINE=83238395; PubMed=6345535;  
RA Kaul R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;  
RT "Amino acid sequence of the N alpha-terminal 201 residues of human  
erythrocyte membrane band 3.";  
RL J. Biol. Chem. 258:7981-7990(1983).  
RN [5]  
RP SEQUENCE OF 1-3.  
RX MEDLINE=79027186; PubMed=701248;  
RA Drickamer L.K.;  
RT "Orientation of the band 3 polypeptide from human erythrocyte  
membranes. Identification of NH2-terminal sequence and site of  
carbohydrate attachment.";  
RL J. Biol. Chem. 253:7242-7248(1978).  
RN [6]  
RP SEQUENCE OF 559-630.  
RX MEDLINE=83308584; PubMed=6615451;  
RA Brock C.J., Tanner M.J.A., Kempf C.;  
RT "The human erythrocyte anion-transport protein. Partial amino acid

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- sequence, conformation and a possible molecular mechanism for anion exchange." J. Biol. Chem. 263:577-586(1988).  
 [7]  
 RA MEDLINE-88228050; PubMed-3372523;  
 RX Kavano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.;  
 RA "Localization of the pyridoxal phosphate binding site at the COOH-  
 RT terminal region of erythrocyte band 3 protein." J. Biol. Chem. 263:8232-8238(1988).  
 RL [8]  
 RN  
 RA ROLE OF GLU-681, AND SEQUENCE OF 665-688.  
 RX MEDLINE-92332495; PubMed-1352774;  
 RX Jennings M.L., Smith J.S.;  
 RA "Anion-proton cotransport through the human red blood cell band 3  
 RT protein. Role of glutamate 681." J. Biol. Chem. 267:13964-13971(1992).  
 RL [9]  
 RN  
 RA PALMITOYLATION OF CYS-843.  
 RX MEDLINE-91358422; PubMed-1885574;  
 RX Okubo K., Hamasaki N., Hara K., Kageura M.;  
 RA "Palmitoylation of cysteine 69 from the COOH-terminal of band 3  
 RT protein in the human erythrocyte membrane. Acylation occurs in the  
 RT middle of the consensus sequence of F-I-IICLAFL found in band 3  
 RT protein and G2 protein of Rift Valley fever virus." J. Biol. Chem. 266:16420-16424(1991).  
 RL [10]  
 RN  
 RA PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.  
 RX MEDLINE-20400020; PubMed-10942405;  
 RX Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E.,  
 RA Pinna L.A., Donella-Deana A.;  
 RA "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine  
 RT kinases in intact human erythrocytes: identification of primary and  
 RT secondary phosphorylation sites." Blood 96:1550-1557(2000).  
 RL [11]  
 RN  
 RA VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-91329825; PubMed-1678289;  
 RX Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delaunay J.,  
 RA Wajman H., Bursaux E.;  
 RA "Human erythrocyte band 3 polymorphism (band 3 Memphis):  
 RT characterization of the structural modification (Lys 56-->Glu) by  
 RT protein chemistry methods." Blood 78:1117-1120(1991).  
 RL [12]  
 RN  
 RA VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-92107882; PubMed-1722314;  
 RX Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,  
 RA Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;  
 RA "Deletion in erythrocyte band 3 gene in malaria-resistant Southeast  
 RT Asian ovalocytosis." Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).  
 RL [13]  
 RN  
 RA VARIANT HS ARG-327.  
 RX MEDLINE-92329950; PubMed-1378323;  
 RX Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,  
 RA Cohen C.M.;  
 RA "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic  
 RT domain of erythrocyte band 3 protein associated with spherocytic  
 RT hemolytic anemia and partial deficiency of protein 4.2." Blood 80:523-529(1992).  
 RL [14]  
 RN  
 RA VARIANT HE 400-ALA--ALA-408 DEL.  
 RX MEDLINE-92167271; PubMed-1538405;  
 RX Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,  
 RA Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,  
 RA Gratzner W.B.;  
 RA "Basis of unique red cell membrane properties in hereditary  
 RT ovalocytosis." J. Mol. Biol. 223:949-958(1992).  
 RL [15]  
 RN  
 RA VARIANT HS LEU-868.  
 RX MEDLINE-93343855; PubMed-8343110;  
 RX
- Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;  
 "Band 3 HT, a human red-cell variant associated with acanthocytosis  
 and increased anion transport, carries the mutation Pro-868-->Leu in  
 the membrane domain of band 3." Biochem. J. 293:317-320(1993).  
 [16]  
 RA VARIANT MONTEFIORE LYS-40.  
 RX MEDLINE-93229758; PubMed-8471774;  
 RX Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,  
 RA Schwartz R.S.;  
 RA "Human erythrocyte protein 4.2 deficiency associated with hemolytic  
 RT anemia and a homozygous 40 glutamic acid-->lysine substitution in the  
 RT cytoplasmic domain of band 3 (band 3Montefiore)." Blood 81:2155-2165(1993).  
 RL [17]  
 RN  
 RA VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.  
 RX MEDLINE-94266802; PubMed-8206915;  
 RX Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;  
 RA "Band 3 Memphis variant II. Altered stilbene disulfonate binding and  
 RT the Diego (Dia) blood group antigen are associated with the human  
 RT erythrocyte band 3 mutation Pro-854-->Leu." J. Biol. Chem. 269:16155-16158(1994).  
 RL [18]  
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 RA VARIANT BLOOD GROUP WR(A).  
 RX MEDLINE-95111140; PubMed-7812009;  
 RX Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,  
 RA Tanner M.J.;  
 RA "Changes in the blood group Wright antigens are associated with a  
 RT mutation at amino acid 658 in human erythrocyte band 3: a site of  
 RT interaction between band 3 and glycophorin A under certain  
 RT conditions." Blood 85:541-547(1995).  
 RL [19]  
 RN  
 RA VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.  
 RX MEDLINE-95134893; PubMed-7530501;  
 RX Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,  
 RA Alper S.L., Brugnara C., Wichterle H., Palek J.;  
 RA "Mutations of conserved arginines in the membrane domain of erythroid  
 RT band 3 lead to a decrease in membrane-associated band 3 and to the  
 RT phenotype of hereditary spherocytosis." Blood 85:634-640(1995).  
 RL [20]  
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 RA VARIANT HS ASP-771.  
 RX MEDLINE-96136073; PubMed-8547122;  
 RX Maillet P., Vallier A., Reinhardt W.H., Wyss E.J., Ott P., Texier P.,  
 RA Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;  
 RA "Band 3 Chur: a variant associated with band 3-deficient hereditary  
 RT spherocytosis and substitution in a highly conserved position of  
 RT transmembrane segment 11." Br. J. Haematol. 91:804-810(1995).  
 RL [21]  
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 RA VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.  
 RX MEDLINE-97099297; PubMed-8943874;  
 RX Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T.,  
 RA Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,  
 RA Palek J.;  
 RA "Characterization of 13 novel band 3 gene defects in hereditary  
 RT spherocytosis with band 3 deficiency." Blood 88:4366-4374(1996).  
 RL [22]  
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 RA VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.  
 RX MEDLINE-96225450; PubMed-8640229;  
 RX Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,  
 RA Dornwell M., Herbers J., Kugler W., Ozcan R., Pekrun A.,  
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 RA "Ankyrin-1 mutations are a major cause of dominant and recessive  
 RT hereditary spherocytosis." Nat. Genet. 13:214-218(1996).  
 RL [23]  
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 RA VARIANTS HS SER-147 AND MET-488.  
 RX MEDLINE-97351102; PubMed-9207478;  
 RX Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon M.,  
 RA Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,

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 DB 742 GKASTPGAAAIQIEVKQRI 761

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 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1).  
 GN SLC4A1 OR AE1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
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 RN [1]  
 RP SEQUENCE OF 46-927 FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=89255254; PubMed=2722777;  
 RA Kudrycki K.E., Shull G.E.;  
 RT "Primary structure of the rat kidney band 3 anion exchange protein  
 deduced from a cDNA";  
 RL J. Biol. Chem. 264:8185-8192(1989).  
 RN [2]  
 RP SEQUENCE OF 1-45 FROM N.A.  
 RA Kudrycki K.E., Shull G.E.;  
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN  
 MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,  
 WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR  
 CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).  
 CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 AND APPEARS TO BE TETRAMERIC.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE  
 BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND  
 COLLECTING DUCTS.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Erythrocyte;  
 CC IsoId=P23562-1; Sequence=Displayed;  
 CC Name=Kidney;  
 CC IsoId=P23562-2; Sequence=VSP\_000455;  
 CC -1- TISSUE SPECIFICITY: Kidney.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: J04793; AAA40800.1; ALT\_INIT.  
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 CC PIR: A33810; A33810.  
 CC HSP: P02730; IRTS.  
 CC InterPro: IPR001717; Anion-exchange.  
 CC InterPro: IPR003020; HCO3 cotranspt.  
 CC Pfam: PF00955; HCO3 cotransp; 1.  
 CC PRINTS: PR01231; HCO3TRANSPO.  
 CC TIGRfams: TIGR00834; ae; 1.  
 CC PROSITE: PS00219; ANION\_EXCHANGER\_1; 1.  
 CC PROSITE: PS00220; ANION\_EXCHANGER\_2; 1.  
 CC Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;

KW Lipoprotein; Palmitate; Alternative splicing.  
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 FT TRANSMEM 421 441 POTENTIAL.  
 FT TRANSMEM 454 473 POTENTIAL.  
 FT TRANSMEM 477 496 POTENTIAL.  
 FT TRANSMEM 508 527 POTENTIAL.  
 FT TRANSMEM 540 558 POTENTIAL.  
 FT DOMAIN 559 585 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 585 604 POTENTIAL.  
 FT DOMAIN 605 619 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 620 640 EXOPLASMIC LOOP (POTENTIAL).  
 FT DOMAIN 641 676 POTENTIAL.  
 FT TRANSMEM 677 696 POTENTIAL.  
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 FT TRANSMEM 860 881 POTENTIAL.  
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Query Match 92.78; Score 89; DB 1; Length 927;  
 Best Local Similarity 95.08; Pred. No. 3.4e-06;  
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QY 1 GKASTPGAAAIQIEVKQRI 20  
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 DB 758 GKASPGAAAIQIEVKQRI 777

RESULT 3  
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 ID B3AT\_MOUSE STANDARD; PRT; 929 AA.  
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 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
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 DE (MEB3).  
 GN SLC4A1 OR AE1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85268011; PubMed=2410791;  
 RA Kopito R.R., Lodish H.F.;  
 RT "Primary structure and transmembrane orientation of the murine anion  
 exchange protein.";  
 RL Nature 316:234-238(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86034211; PubMed=3840489;  
 RA Kopito R.R., Lodish H.F.;  
 RT "Structure of the murine anion exchange protein.";  
 RL J. Cell. Biochem. 29:1-17(1985).  
 RN [3]  
 RP PARTIAL SEQUENCE FROM N.A.  
 RX MEDLINE=87250387; PubMed=3036795;  
 RA Kopito R.R., Andersson M., Lodish H.F.;  
 RT "Structure and organization of the murine band 3 gene.";  
 RL J. Biol. Chem. 262:8035-8040(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Kopito R.R.;  
 RL Submitted (JUL-1987) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 11-929 FROM N.A.  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:25:42 ; Search time 9.25 Seconds  
(without alignments)  
101.679 Million cell updates/sec

Title: US-10-087-464-4

Perfect score: 112  
Sequence: 1 DRILLFKPKYHPDPYVK 20

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	108	96.4	927	1	B3AT_HUMAN
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4	82	73.2	922	1	B3AT_CHICK
5	74	66.1	1234	1	B3AT_RAT
6	74	66.1	1237	1	B3A2_MOUSE
7	74	66.1	1237	1	B3A2_RABIT
8	74	66.1	1241	1	B3A2_HUMAN
9	73	65.2	1238	1	B3A2_CAVPO
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19	49	43.8	469	1	PPAF_ARATH
20	48	42.9	403	1	STAL_MOUSE
21	47.5	42.4	304	1	WBPI_MOUSE
22	47	42.0	168	1	CYNS_ORYSA
23	47	42.0	234	1	YB46_METHV
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25	46	41.1	218	1	VNS3_AHSV2
26	46	41.1	218	1	VNS3_AHSV8
27	46	41.1	578	1	HPCL_HUMAN
28	45	40.2	403	1	STAL_RAT
29	45	40.2	406	1	STAL_HUMAN
30	45	40.2	434	1	NO75_LUPLU
31	45	40.2	588	1	DNLI_THEVO
32	45	40.2	859	1	DM3B_MOUSE
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					P29712 anabaena sp

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38	43.5	38.8	1268	1	VGLN_HUMAN
39	43.5	38.8	1270	1	VGLN_CHICK
40	43	38.4	238	1	E6_GOSHI
41	43	38.4	248	1	GRAN_GVTN
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43	43	38.4	324	1	LEG4_RAT
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## ALIGNMENTS

RESULT 1  
B3AT\_HUMAN  
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DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
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DE (CD233 antigen).  
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RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90083213; PubMed=2594752;  
RA Lux S.E., John K.M., Kopito R.R., Lodish H.F.;  
RT "Cloning and characterization of band 3, the human erythrocyte anion-exchange protein (AE1).";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=89134172; PubMed=3223947;  
RA Tanner M.J.A., Martin P.G., High S.;  
RT "The complete amino acid sequence of the human erythrocyte membrane anion-transport protein deduced from the cDNA sequence.";  
RL Biochem. J. 256:703-712(1988).  
RN [3]  
RP SEQUENCE OF 1-199; 220-292 AND 347-370.  
RX MEDLINE=90001294; PubMed=2790053;  
RA Yannoukakis D., Vasseur C., Blouquit Y., Bursaux E., Wajzman H.;  
RT "Primary structure of the cytoplasmic domain of human erythrocyte protein band 3. Comparison with its sequence in the mouse.";  
RL Biochim. Biophys. Acta 998:43-49(1989).  
RN [4]  
RP SEQUENCE OF 1-201.  
RX MEDLINE=83238395; PubMed=6345535;  
RA Kaul R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;  
RT "Amino acid sequence of the N alpha-terminal 201 residues of human erythrocyte membrane band 3";  
RL J. Biol. Chem. 258:7981-7990(1983).  
RN [5]  
RP SEQUENCE OF 1-3.  
RX MEDLINE=79027186; PubMed=701248;  
RA Drickamer L.K.;  
RT "Orientation of the band 3 polypeptide from human erythrocyte membranes. Identification of NH2-terminal sequence and site of carbohydrate attachment.";  
RL J. Biol. Chem. 253:7242-7248(1978).  
RN [6]  
RP SEQUENCE OF 559-630.  
RX MEDLINE=83308584; PubMed=6615451;  
RA Brock C.J., Tanner M.J.A., Kempf C.;  
RT "The human erythrocyte anion-transport protein. Partial amino acid

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Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;  
"band 3 HT, a human red-cell variant associated with acanthocytosis  
RT and increased anion transport, carries the mutation Pro-868-->Leu in  
RT the membrane domain of band 3."  
RL Biochem. J. 293:317-320(1993).  
RN [16]  
RP VARIANT MONTEFIORE LYS-40.  
RX MEDLINE=93229758; PubMed=84711774;  
RA Rydicki A.C., Olu J.J.H., Musto S., Rosen N.L., Nagel R.L.,  
RA Schwartz R.S.;  
RA "Human erythrocyte protein 4.2 deficiency associated with hemolytic  
RT anemia and a homozygous 40 glutamic acid-->lysine substitution in the  
RT cytoplasmic domain of band 3 (band 3Montefiore).";  
RL Blood 81:2155-2165(1993).  
RN [17]  
RP VARIANT BLOOD GROUP DI(A)(MEMPHIS-II).  
RX MEDLINE=94266802; PubMed=8206915;  
RA Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;  
RA "band 3 Memphis variant II. Altered stilbene disulfonate binding and  
RT the Diego (Dia) blood group antigen are associated with the human  
RT erythrocyte band 3 mutation pro-854-->Leu.";  
RL J. Biol. Chem. 269:16155-16158(1994).  
RN [18]  
RP VARIANT BLOOD GROUP WR(A).  
RX MEDLINE=95111140; PubMed=7812009;  
RA Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,  
RA Tanner M.J.;  
RA "Changes in the blood group Wright antigens are associated with a  
RT mutation at amino acid 658 in human erythrocyte band 3: a site of  
RT interaction between band 3 and glycophorin A under certain  
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RP VARIANTS HS GLN-760; TRP-760; CVS-808 AND TRP-870.  
RX MEDLINE=95134893; PubMed=7530501;  
RA Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,  
RA Alper S.L., Brugnara C., Wichterle H., Palek J.;  
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RT band 3 lead to a decrease in membrane-associated band 3 and to the  
RT phenotype of hereditary spherocytosis.";  
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RX MEDLINE=96136073; PubMed=8547122;  
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RA Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;  
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RX MEDLINE=97099297; PubMed=8943874;  
RA Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T.,  
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RT spherocytosis with band 3 deficiency.";  
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RT hereditary spherocytosis.";  
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RP VARIANTS HS SER-147 AND MET-488.  
RX MEDLINE=97351102; PubMed=9207478;  
RA Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon M.,  
RA Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.

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Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 807 DRILLFKPKYHPDVPYVK 826

RESULT 2
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ID B3AT_RAT STANDARD; PRT; 927 AA.
AC P23562;
DT 01-NOV-1991 (Rel. 20, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
GN SLC4A1 OR AEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 46-927 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=89255254; PubMed=2722777;
RA Kudrycki K.E., Shull G.E.;
RT "Primary structure of the rat kidney band 3 anion exchange protein
   deduced from a cDNA";
RL J. Biol. Chem. 264:8185-8192(1989).
RN [2]
RP SEQUENCE OF 1-45 FROM N.A.
RA Kudrycki K.E., Shull G.E.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
   MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
   WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
   CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).
CC -!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
   AND APPEARS TO BE TETRAMERIC.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
   BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
   COLLECTING DUCTS.
CC -!- ALTERNATIVE PRODUCTS:
   Event=Alternative splicing; Named isoforms=2;
   Name=Erythrocyte;
   IsoId=P23562-1; Sequence=Displayed;
   Name=Kidney;
   IsoId=P23562-2; Sequence=VSP_000455;
CC -!- TISSUE SPECIFICITY: Kidney.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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or send an email to license@isb-sib.ch).
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DR EMBL; L02943; AAA40801.1; -.
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DR HSSP; P02730; 1BFS.
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DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp. 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
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DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;

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Lipoprotein; Palmitate; Alternative splicing.
KW DOMAIN 1 420 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 421 927 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 421 441 POTENTIAL.
FT TRANSMEM 454 473 POTENTIAL.
FT TRANSMEM 477 496 POTENTIAL.
FT TRANSMEM 508 527 POTENTIAL.
FT TRANSMEM 540 558 POTENTIAL.
FT DOMAIN 559 585 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 585 604 POTENTIAL.
FT DOMAIN 605 619 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 620 640 POTENTIAL.
FT DOMAIN 641 676 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 677 696 POTENTIAL.
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FT TRANSMEM 801 822 POTENTIAL.
FT TRANSMEM 860 881 POTENTIAL.
FT CARBOHYD 658 658 N-LINKED (GLCNAC... ) (PROBABLE).
FT LIPID 859 859 PALMITATE (BY SIMILARITY).
FT VARSPLIC 1 79 Missing (in isoform kidney).
FT /FTID=VSP_000455.
SQ SEQUENCE 927 AA; 103172 MW; 681A328474E5E9DE CRC64;

Query Match      96.4%; Score 108; DB 1; Length 927;
Best Local Similarity 95.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDVPYVK 20
    |||||
Db 823 DRILLFKPKYHPDVPYVK 842

RESULT 3
B3AT_MOUSE
ID B3AT_MOUSE STANDARD; PRT; 929 AA.
AC P04919;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
   (MEB3).
GN SLC4A1 OR AEL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85268011; PubMed=2410791;
RA Kopito R.R., Lodish H.F.;
RT "Primary structure and transmembrane orientation of the murine anion
   exchange protein.";
RL Nature 316:234-238(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86034211; PubMed=3840489;
RA Kopito R.R., Lodish H.F.;
RT "Structure of the murine anion exchange protein.";
RL J. Cell. Biochem. 29:1-17(1985).
RN [3]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=87250387; PubMed=3036795;
RA Kopito R.R., Andersson M., Lodish H.F.;
RT "Structure and organization of the murine band 3 gene.";
RL J. Biol. Chem. 262:8035-8040(1987).
RN [4]
RP SEQUENCE FROM N.A.
RA Kopito R.R.;
RL Submitted (JUL-1987) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 11-929 FROM N.A.
RX MEDLINE=86274622; PubMed=3015590;

```

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RA Demuth D.R., Shove L.C., Ballantine M., Palumbo A., Fraser P.J.,  
RA Cioe L., Rovera G., Curtis P.J.;  
RT "Cloning and structural characterization of a human non-erythroid  
RT band 3-like protein.";  
RL EMBO J. 5:1205-1214(1986).  
RN [6]  
RP SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.  
RX MEDLINE=89229233; PubMed=2713407;  
RA Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,  
RA Passow H.;  
RT "Major proteolytic fragments of the murine band 3 protein as obtained  
RT after in situ proteolysis";  
RL Biochim. Biophys. Acta 980:291-298(1989).  
CC -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE  
CC ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS  
CC INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS  
CC THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING  
CC SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND  
CC HEMOGLOBIN.  
CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
CC AND APPEARS TO BE TETRAMERIC.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name=Erythrocyte;  
CC IsoId=P04919-1; Sequence=Displayed;  
CC Name=Kidney;  
CC IsoId=P04919-2; Sequence=VSP\_000454;  
CC -1- TISSUE SPECIFICITY: ERYTHROCYTE  
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X02677; CAA26506.1; -  
CC EMBL; M29379; AAA37187.1; -  
CC EMBL; J02756; AAA37278.1; -  
CC EMBL; X03917; CAA27555.1; -  
CC PIR; A25314; A25314.  
CC HSP; P02730; IRTS.  
CC MGD; MGI:109393; Slc4a1.  
DR InterPro; IPR001717; Anion\_exchange.  
DR Pfam; PF00955; HCO3\_cotransp.  
DR PRINTS; PR01231; HCO3TRNSPORT.  
DR TIGRFS; TIGR00834; ae; 1.  
DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;  
KW Lipoprotein; Palmitate; Alternative splicing.  
FT DOMAIN 1 422 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).  
FT TRANSMEM 423 443 POTENTIAL.  
FT TRANSMEM 456 475 POTENTIAL.  
FT TRANSMEM 479 498 POTENTIAL.  
FT TRANSMEM 510 529 POTENTIAL.  
FT TRANSMEM 542 560 POTENTIAL.  
FT DOMAIN 561 586 EXOPLASMIC LOOP (POTENTIAL).  
FT TRANSMEM 587 606 POTENTIAL.  
FT DOMAIN 607 621 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 622 642 POTENTIAL.  
FT DOMAIN 643 678 EXOPLASMIC LOOP (POTENTIAL).  
FT TRANSMEM 679 698 POTENTIAL.  
FT TRANSMEM 717 737 POTENTIAL.  
FT TRANSMEM 781 798 POTENTIAL.  
FT TRANSMEM 803 824 POTENTIAL.  
FT TRANSMEM 862 883 POTENTIAL.  
FT CARBOHYD 660 N-LINKED (GLCNAC, . .) (PROBABLE).

FT LIPID 861 861 PALMITATE (BY SIMILARITY).  
FT VARSPLIC 1 79 Missing (In isoform Kidney).  
FT CONFLICT 467 467 /FTid=VSP\_000454.  
FT SEQUENCE 929 AA; 103135 MW; 5C0E281C394FB614 CRC64;  
G->S (IN REF. 5).  
Query Match 96.4%; Score 108; DB 1; Length 929;  
Best Local Similarity 95.0%; Pred. No. 1.3e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 DRILLFKPKYHPDVPYVK 20  
Db 825 DRILLFKPKYHPDVPYVK 844  
|||||  
RESULT 4  
B3AT\_CHICK STANDARD; PRT; 922 AA.  
ID B3AT\_CHICK  
AC P15575;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Band 3 anion transport protein.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OC NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89039870; PubMed=3185555;  
RA Kim H.R.C., Vew N.S., Anseorge W., Voss H., Schwager C.,  
RA Vennstrom B., Zenke M., Engel J.D.;  
RT "Two different mRNAs are transcribed from a single genomic locus  
RT encoding the chicken erythrocyte anion transport proteins (band 3)."  
RL Mol. Cell. Biol. 8:4416-4424(1988).  
CC -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE  
CC ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS  
CC INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS  
CC THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING  
CC SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND  
CC HEMOGLOBIN.  
CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
CC AND APPEARS TO BE TETRAMERIC.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: ERYTHROCYTE.  
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M23404; AAA48753.1; -  
CC HSP; P02730; IRTS.  
DR InterPro; IPR001717; Anion\_exchange.  
DR Pfam; PF00955; HCO3\_cotransp.  
DR PRINTS; PR01231; HCO3TRNSPORT.  
DR TIGRFS; TIGR00834; ae; 1.  
DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;  
FT DOMAIN 1 416 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 417 922 MEMBRANE (ANION EXCHANGE).  
FT TRANSMEM 417 437 POTENTIAL.  
FT TRANSMEM 450 469 POTENTIAL.  
FT TRANSMEM 473 492 POTENTIAL.  
FT TRANSMEM 504 523 POTENTIAL.  
FT TRANSMEM 536 554 POTENTIAL.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:41:03 ; Search time 17.25 Seconds  
(without alignments)  
111.500 Million cell updates/sec

Title: US-10-087-464-1

Perfect score: 104

Sequence: 1 GMPWLSATTVRSVTHANALT 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

hed: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	848	2 A33810	band 3 anion trans
2	104	100.0	911	1 B3HU	band 3 anion trans
3	104	100.0	929	2 A25314	band 3 protein - m
4	100	96.2	844	2 I50159	anion transporter
5	100	96.2	922	2 A30816	band 3 anion trans
6	95	91.3	912	2 S59861	band 3 anion trans
7	95	91.3	918	2 S24318	band 3 anion trans
8	93	89.4	865	2 A25104	band 3 protein, no
9	93	89.4	1234	2 A34911	band 3-related pro
10	93	89.4	1237	2 A31789	band 3-related pro
11	93	89.4	1237	2 A36764	band 3-related pro
12	93	89.4	1240	2 T21086	anion exchange pro
13	89	85.6	1030	2 A42497	anion exchanger 3,
14	89	85.6	1227	2 B34911	band 3-related pro
15	89	85.6	1227	2 A33638	erythrocyte anion
16	89	85.6	1232	2 I38496	anion exchanger 3
17	84	80.8	357	2 S31828	band 3 anion trans
18	53	51.0	826	2 T28858	hypothetical prote
19	48	45.2	314	2 T44895	probable lipoid ac
20	47	45.2	1035	2 T31336	sodium bicarbonate
21	47	45.2	1035	2 T13962	sodium bicarbonate
22	47	45.2	1035	2 T14110	sodium bicarbonate
23	47	45.2	1079	2 PC7034	Na+ bicarbonate co
24	47	45.2	1079	2 T14031	sodium bicarbonate
25	46	44.2	156	2 C72506	hypothetical prote
26	45	43.3	111	2 B72722	hypothetical prote
27	45	43.3	302	2 F69000	cobalamin biosynth
28	45	43.3	727	2 A56879	diacylglycerol kin
29	45	43.3	1119	2 T37460	probable sodium bi

30	45	43.3	1175	2 T22491	hypothetical prote
31	44	42.3	449	2 H70526	probable cytochrom
32	44	42.3	1508	2 T27828	hypothetical prote
33	44	42.3	1519	2 T27829	hypothetical prote
34	43	41.3	115	2 T11840	NADH2 dehydrogenas
35	43	41.3	305	2 D83699	hypothetical prote
36	43	41.3	311	2 C70787	probable lipoid ac
37	43	41.3	387	2 T22841	hypothetical prote
38	43	41.3	415	2 T42379	phO85-like protein
39	43	41.3	431	1 UKHU	u-plasminogen acti
40	42.5	40.9	552	1 E57987	cytochrome c-type
41	42.5	40.9	552	2 D86101	hypothetical prote
42	42.5	40.9	552	2 H91260	cytochrome c-type
43	42	40.4	332	2 T45065	iron binding prote
44	42	40.4	350	2 D83563	hypothetical prote
45	42	40.4	354	1 MMECPW	glycine betaine/L-

ALIGNMENTS

RESULT 1

A33810

band 3 anion transport protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Aug-1999

C:Accession: A33810

R:Kudrycki, K.E.; Shull, G.E.

J. Biol. Chem. 264, 8185-8192, 1989

A:Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr

A:Reference number: A33810; MUID:8925254; PMID:2722777

A:Accession: A33810

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-848 <RUD>

A:Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093

C:Superfamily: band 3 anion transport protein

C:Keywords: alternative splicing; transmembrane protein

Query Match 100.0%; Score 104; DB 2; Length 848;

Best Local Similarity 100.0%; Pred. No. 8.3e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

1 GMPWLSATTVRSVTHANALT 20

Db

657 GMPWLSATTVRSVTHANALT 676

RESULT 2

B3HU

band 3 anion transport protein, erythrocyte - human

N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha

C:Species: Homo sapiens (man)

C>Date: 03-Aug-1984 #sequence\_revision 03-Oct-1995 #text\_change 22-Jun-1999

C:Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079;

R:Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.

Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989

A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange

A:Reference number: A36218; MUID:90083213; PMID:2594752

A:Accession: A36218

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-911 <LUX>

A:Cross-references: GB:M27819; NID:gl78215; PIDN:AAA35514.1; PID:gl78216

R:Tanner, M.J.A.; Martin, P.G.; High, S.

Biochem. J. 256, 703-712, 1988

A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra

A:Reference number: S03074; MUID:89134172; PMID:3223947

A:Accession: S03074

A:Molecule type: mRNA

A:Residues: 1-55, 'E', 'Y', '911 <TAN>

A:Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714

R:Shove, L.C.; Ballantine, M.; Huebner, K.

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Genomics 1, 71-76, 1987  
 A>Title: Localization of the gene for the erythroid anion exchange protein, band 3 (EMPE)  
 A:Reference number: I39408; MUID:88031311; PMID:3478298  
 A:Accession: I39408  
 A:Molecule type: DNA  
 A:Residues: 37-56 <SHOI>  
 A:Cross-references: GB:M16978; NID:gl78217; PIDN:AAA51670.1; PID:gl78220  
 A:Accession: I39409  
 A:Molecule type: DNA  
 A:Residues: 118-161 <SHO2>  
 A:Cross-references: GB:M16979; NID:gl78218; PIDN:AAA51671.1; PID:g553169  
 R:Drickamer, L.K.  
 J. Biol. Chem. 253, 7242-7248, 1978  
 A>Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Identif  
 A:Reference number: A92237; MUID:79027186; PMID:701248  
 A:Accession: A92237  
 A:Molecule type: protein  
 A:Residues: 1-3 <DRI>  
 R:Wady, W.J.; Findlay, J.B.C.  
 J. Biol. Chem. 255, 465-475, 1982  
 A>Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-bin  
 A:Reference number: A26507; MUID:83074521; PMID:7150226  
 A:Accession: A26507  
 A:Molecule type: protein  
 A:Residues: 360-364, 'D', 366-369 <MAW>  
 R:Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.  
 J. Biol. Chem. 258, 7981-7990, 1983  
 A>Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte  
 A:Reference number: A92430; MUID:83338395; PMID:6345535  
 A:Accession: A92430  
 A:Molecule type: protein  
 A:Residues: 1-10, 'D', 12-68, 'E', 69-200 <KAU>  
 R:Brock, C.J.; Tanner, M.J.A.; Kempf, C.  
 Biochem. J. 213, 577-586, 1983  
 A>Title: The human erythrocyte anion-transport protein.  
 A:Reference number: A90323; MUID:83308584; PMID:6615451  
 A:Accession: A90323  
 A:Molecule type: protein  
 A:Residues: 559-630 <BRO>  
 R:Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.  
 J. Biol. Chem. 263, 8232-8238, 1988  
 A>Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regio  
 A:Reference number: A28079; MUID:88228050; PMID:3372523  
 A:Accession: A28079  
 A:Molecule type: protein  
 A:Residues: 834-842, 'X', 844-911 <KAN>  
 Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate fo  
 R:Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.  
 Biochim. Biophys. Acta 998, 43-49, 1989  
 A>Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3  
 A:Reference number: S05523; MUID:90001294; PMID:2790053  
 A:Accession: S05523  
 A:Molecule type: protein  
 A:Residues: 1-201;220-292;307-308, 'R', 310-312, 'S', 314-329, 'K', 331-333;347-370 <YAN1>  
 R:Cobb, C.E.; Beth, A.H.  
 Biochemistry 29, 8283-8290, 1990  
 A>Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyt  
 A:Reference number: A35835; MUID:91070049; PMID:1701324  
 A:Accession: A35835  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 361-364, 'X', 366-372;424-429, 'X', 431-434 <COB>  
 A:Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes  
 R:Yannoukakos, D.; Vasseur, C.; Drancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.;  
 Blood 78, 1117-1120, 1991  
 A>Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the  
 A:Reference number: A44933; MUID:91329825; PMID:1678289  
 A:Accession: A44933  
 A:Molecule type: protein  
 A:Residues: 1-55, 'E', 57-69 <YAN2>  
 Note: sequence extracted from NCBI backbone (NCBIP:49829)  
 Note: sequence of a common polymorphic form designated band 3 Memphis

A:Referenc  
 A:Accessio  
 A:Molecul

R:Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.  
 J. Biol. Chem. 267, 19211-19217, 1992  
 A>Title: A structural study of the membrane domain of band 3 by tryptic digestion. Co  
 A:Reference number: A44116; MUID:92406862; PMID:1527044  
 A:Accession: A44116  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <  
 A:Experimental source: erythrocyte  
 A:Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:1138  
 A:Note: a histidine residue essential for anion transport is suggested to be His-651,  
 R:Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.  
 J. Biol. Chem. 269, 1918-1926, 1994  
 A>Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS  
 A:Reference number: A49717; MUID:94124538; PMID:8294441  
 A:Accession: A49717  
 A:Molecule type: protein  
 A:Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>  
 A:Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transpo  
 R:Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.  
 J. Biochem. 122, 577-585, 1997  
 A>Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: F1  
 A:Reference number: PC4403; MUID:98006310; PMID:9348087  
 A:Accession: PC4403  
 A:Molecule type: protein  
 A:Residues: 361-911 <HAM>  
 C:Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A d  
 C:Comment: Band 3 has at least two functional domains. Its integral domain mediates a  
 ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.  
 C:Genetics:  
 A:Gene: GDB:SLC4A1; EPB3  
 A:Cross-references: GDB:119874; OMIM:109270  
 A:Map position: 17q21-17q22  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm  
 F:1-403/Region: cytoskeletal protein binding  
 F:404-911/Region: anion antiporter  
 F:405-427/Domain: transmembrane #status predicted <TM01>  
 F:433-457/Domain: transmembrane #status predicted <TM02>  
 F:459-479/Domain: transmembrane #status predicted <TM03>  
 F:491-507/Domain: transmembrane #status predicted <TM04>  
 F:522-542/Domain: transmembrane #status predicted <TM05>  
 F:568-588/Domain: transmembrane #status predicted <TM06>  
 F:604-624/Domain: transmembrane #status predicted <TM07>  
 F:659-680/Domain: transmembrane #status predicted <TM08>  
 F:701-721/Domain: transmembrane #status predicted <TM09>  
 F:723-743/Domain: transmembrane #status predicted <TM10>  
 F:764-780/Domain: transmembrane #status predicted <TM11>  
 F:785-806/Domain: transmembrane #status predicted <TM12>  
 F:839-859/Domain: transmembrane #status predicted <TM13>  
 F:861-881/Domain: transmembrane #status predicted <TM14>  
 F:1/Modified site: acetylated amino end (Met) #status experimental  
 F:539,590,851/Binding site: anion (Lys) #status experimental  
 F:642/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.08; Score 104; DB 1; Length 911;  
 Best Local Similarity 100.08; Pred. No. 9e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVSRTVTHANALT 20  
 |||||  
 DB 720 GMPWLSATTVSRTVTHANALT 739

RESULT 3

band 3 protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Aug-1999

C:Accession: A25314; A26086; I49524; B25104

R:Kopito, R.R.; Lodish, H.F.

A>Title: Primary structure and transmembrane orientation of the murine anion exchange

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A:Accession: A25314  
 A:Reference number: A25314; MUID:85268011; PMID:2410791  
 A:Molecule type: mRNA  
 A:Residues: 1-929 <KOP>  
 A:Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898  
 R:Kopito, R.R.; Lodish, H.F.  
 J. Cell. Biochem. 29, 1-17, 1985  
 A:Title: Structure of the murine anion exchange protein.  
 A:Reference number: A26086; MUID:86034211; PMID:3840489  
 A:Accession: A26086  
 A:Molecule type: mRNA  
 A:Residues: 1-929 <KO2>  
 A:Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742  
 R:Kopito, R.R.; Anderson, M.; Lodish, H.F.  
 J. Biol. Chem. 262, 8035-8040, 1987  
 A:Title: Structure and organization of the murine band 3 gene.  
 A:Reference number: I49524; MUID:87250387; PMID:3036795  
 A:Accession: I49524  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 4-707, 'X', 709-902 <RES>  
 A:Cross-references: GB:J02756; PIDN:AAA37278.1; PID:g553874  
 R:Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera  
 EMO J. 5, 1205-1214, 1986  
 A:Title: Cloning and structural characterization of a human non-erythroid band 3-like pr  
 A:Reference number: A91039; MUID:86274622; PMID:3015590  
 A:Accession: B25104  
 A:Molecule type: mRNA  
 A:Residues: 11-466, 'S', 468-929 <DEM>  
 A:Cross-references: GB:X03917; NID:g53042; PIDN:CAA27555.1; PID:g53043  
 C:Genetics:  
 A:Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/  
 A:Superfamily: band 3 anion transport protein  
 C:Keywords: transmembrane protein

Query Match 100.0%; Score 104; DB 2; Length 929;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
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 Db 738 GMPWLSATTVRSVTHANALT 757

RESULT 4  
 50159  
 Anion transporter - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 20-Aug-1999  
 C:Accession: I50159  
 R:Cox, J.V.; Lazarides, E.  
 Mol. Cell. Biol. 8, 1327-1335, 1988  
 A:Title: Alternative primary structures in the transmembrane domain of the chicken eryth  
 A:Reference number: I50159; MUID:88216609; PMID:2835670  
 A:Accession: I50159  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-844 <COX>  
 A:Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212  
 C:Superfamily: band 3 anion transport protein

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 Best Local Similarity 90.0%; Pred. No. 3.7e-08;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
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 Db 653 GMPWLSATTVRVTTHANALT 672

RESULT 5  
 A30816  
 band 3 anion transport protein (clone pBIIIC1) - chicken

C:Species: Gallus gallus (chicken)  
 C:Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 16-Feb-1997  
 C:Accession: A30816  
 R:Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke,  
 Mol. Cell. Biol. 8, 4416-4424, 1988  
 A:Title: Two different mRNAs are transcribed from a single genomic locus encoding the  
 A:Reference number: A30816; MUID:89039870; PMID:3185555  
 A:Accession: A30816  
 A:Molecule type: mRNA  
 A:Residues: 1-922 <KIM>  
 A:Cross-references: GB:M23404  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: transmembrane protein

Query Match 96.28; Score 100; DB 2; Length 922;  
 Best Local Similarity 90.0%; Pred. No. 4.1e-08;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
 |||||  
 Db 731 GMPWLSATTVRVTTHANALT 750

RESULT 6  
 S59861  
 band 3 anion transport protein isoform b - rainbow trout  
 C:Species: Oncorhynchus mykiss (rainbow trout)  
 C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Aug-1999  
 C:Accession: S59861  
 R:Fleivet, B.; Gabillat, N.; Borgese, F.; Motaïs, R.  
 EMO J. 14, 5158-5169, 1995  
 A:Title: Expression of band 3 anion exchanger induces chloride current and taurine tr  
 A:Reference number: S59861; MUID:96080151; PMID:7489705  
 A:Accession: S59861  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-912 <FIE>  
 A:Cross-references: EMBL:Z50848; NID:g1004316; PIDN:CAA90701.1; PID:g1004317  
 C:Superfamily: band 3 anion transport protein

Query Match 91.3%; Score 95; DB 2; Length 912;  
 Best Local Similarity 90.0%; Pred. No. 2.7e-07;  
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
 |||||  
 Db 727 GMPWLSATTVRSVTHANALT 746

RESULT 7  
 S24318  
 band 3 anion transport protein - rainbow trout  
 C:Species: Oncorhynchus mykiss (rainbow trout)  
 C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Aug-1999  
 C:Accession: S24318; S36083; S22173  
 R:Huebner, S.; Michel, F.; Rudloff, V.; Appelhaus, H.  
 Biochem. J. 285, 17-23, 1992  
 A:Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes deriv  
 A:Reference number: S24318; MUID:92344566; PMID:1637296  
 A:Accession: S24318  
 A:Molecule type: mRNA  
 A:Residues: 1-918 <HUE1>  
 A:Cross-references: EMBL:X61699  
 A:Accession: S36083  
 A:Molecule type: protein  
 A:Residues: 71-89; 94-114; 570-588 <HUE2>  
 R:Appelhaus, H.  
 submitted to the EMBL Data Library, August 1991  
 A:Reference number: S22173  
 A:Accession: S22173  
 A:Molecule type: mRNA  
 A:Residues: 1-304, 'G', 306-918 <APP>  
 A:Cross-references: EMBL:X61699; NID:g64308; PIDN:CAA43868.1; PID:g64309

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:41:03 ; Search time 17.25 Seconds  
(without alignments)  
111.500 Million cell updates/sec

Title: US-10-087-464-2  
Perfect score: 98  
Sequence: 1 SVTHANALVVGKASTPGAA 20  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	911	1 B3HU	band 3 anion trans
2	91	92.9	848	2 A33810	band 3 anion trans
3	91	92.9	929	2 A25314	band 3 protein - m
4	73	74.5	865	2 A25104	band 3-related pro
5	73	74.5	1234	2 A34911	band 3-related pro
6	73	74.5	1237	2 A31789	band 3-related pro
7	73	74.5	1237	2 A56764	band 3-related pro
8	73	74.5	1240	2 S21086	anion exchange pro
9	71	72.4	844	2 I50359	anion transporter
10	71	72.4	922	2 A30816	band 3 anion trans
11	63	64.3	912	2 S59861	band 3 anion trans
12	63	64.3	918	2 S24318	band 3 anion trans
13	61	62.2	1030	2 A42497	anion exchanger 3,
14	61	62.2	1227	2 B34911	band 3-related pro
15	61	62.2	1227	2 A33638	erythrocyte anion
16	61	62.2	1232	2 I38496	anion exchanger 3
17	57	58.2	357	2 S31828	band 3 anion trans
18	49	50.0	262	2 I64139	hypothetical prote
19	48	49.0	1655	2 E97835	probable ferredoxi
20	47.5	48.5	409	2 H95911	outer membrane pro
21	47	48.0	1300	2 S07575	proline dehydrogen
22	45	45.9	1127	2 T28435	transferrase homolo
23	44	44.9	407	2 T30585	nucleolin - human
24	42.5	43.4	707	2 A35804	cell division prot
25	42	42.9	303	2 B71638	probable transcrip
26	42	42.9	343	2 E95911	basic leucine zipp
27	42	42.9	422	2 T09120	hypothetical prote
28	42	42.9	1213	2 T19835	hypothetical prote
29	42	42.9	1616	2 T47801	hypothetical prote

ALIGNMENTS

RESULT 1

B3HU  
band 3 anion transport protein, erythrocyte - human  
N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion exch-  
C:Species: Homo sapiens (man)  
C>Date: 03-Aug-1984 #sequence.revision 03-Oct-1995 #text\_change 22-Jun-1999  
C;Accession: A36218; S03074; I39408; I39409; A32237; A26507; A92430; A90323; A28079;  
R;Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989  
A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchang-  
A:Reference number: A36218; MUID:90083213; PMID:2594752  
A:Accession: A36218  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-911 <LUX>  
A:Cross-references: GB:M27819; NID:gl78215; PIDN:AAA35514.1; PID:gl78216  
R;Tanner, M.J.A.; Martin, P.G.; High, S.  
Biochem. J. 256, 703-712, 1988  
A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-tr  
A:Reference number: S03074; MUID:89134172; PMID:3223947  
A:Accession: S03074  
A:Molecule type: mRNA  
A:Residues: 1-55, 'E', 57-911 <TAN>  
A:Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714  
R;Showe, L.C.; Ballantine, M.; Huebner, K.  
Genomics 1, 71-76, 1987  
A:Title: Localization of the gene for the erythroid anion exchange protein, band 3 (  
A:Reference number: I39408; MUID:88031311; PMID:3478298  
A:Accession: I39408  
A:Molecule type: DNA  
A:Residues: 37-56 <SHOL>  
A:Cross-references: GB:M16978; NID:gl78217; PIDN:AAA51670.1; PID:gl78220  
A:Accession: I39409  
A:Molecule type: DNA  
A:Residues: 118-161 <SHO2>  
A:Cross-references: GB:M16979; NID:gl78218; PIDN:AAA51671.1; PID:g553169  
R;Drickamer, L.K.  
J. Biol. Chem. 253, 7242-7248, 1978  
A:Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Ide  
A:Reference number: A92237; MUID:79027186; PMID:701248  
A:Accession: A92237  
A:Molecule type: protein  
A:Residues: 1-3 <DRI>  
R;Mawby, W.J.; Findlay, J.B.C.  
Biochem. J. 205, 465-475, 1982  
A:Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate  
A:Reference number: A26507; MUID:83074521; PMID:7150226  
A:Accession: A26507  
A:Molecule type: protein  
A:Residues: 437-473; 360-364, 'D', 366-369 <MAW>  
R;Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.  
J. Biol. Chem. 258, 7981-7990, 1983

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A:Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte  
A:Reference number: A92430; MUID:83238395; PMID:634535  
A:Accession: A92430  
A:Molecule type: protein  
A:Residues: 1-10, 'D', '12-68, 'E', '69-200 <KAW>  
R:Brook, C.J.; Tanner, M.J.A.; Kempf, C.  
Biochem. J. 213, 577-586, 1983  
A:Title: The human erythrocyte anion-transport protein.  
A:Reference number: A90323; MUID:83308584; PMID:8613451  
A:Accession: A90323  
A:Molecule type: protein  
A:Residues: 559-630 <BRO>  
A:Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport  
R:Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.  
J. Biol. Chem. 263, 8232-8238, 1988  
A:Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal region  
A:Reference number: A28079; MUID:86228050; PMID:3372523  
A:Accession: A28079  
A:Molecule type: protein  
A:Residues: 834-842, 'X', '844-911 <KAW>  
A:Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate for  
R:Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.  
Biochim. Biophys. Acta 998, 43-49, 1989  
A:Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3  
A:Reference number: S05523; MUID:90001294; PMID:2790053  
A:Accession: S05523  
A:Molecule type: protein  
A:Residues: 1-201, 220-292; 307-308, 'R', '310-312, 'S', '314-329, 'K', '331-333; 347-370 <YAN1>  
R:Cobb, C.E.; Beth, A.H.  
Biochemistry 29, 8283-8290, 1990  
A:Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyte  
A:Reference number: A35835; MUID:91070049; PMID:1701324  
A:Accession: A35835  
A:Molecule type: protein  
A:Residues: 361-364, 'X', '366-372; 424-429, 'X', '431-434 <COB>  
A:Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes  
R:Yannoukakos, D.; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.  
Blood 78, 1117-1120, 1991  
A:Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the  
A:Reference number: A4933; MUID:91329825; PMID:1678289  
A:Accession: A4933  
A:Molecule type: protein  
A:Residues: 1-55, 'E', '57-69 <YAN2>  
A:Note: sequence extracted from NCBI backbone (NCBIP:49829)  
R:Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.  
J. Biol. Chem. 267, 19211-19217, 1992  
A:Title: A structural study of the membrane domain of band 3 by tryptic digestion. Conf  
A:Reference number: A4416; MUID:92406862; PMID:1527044  
A:Accession: A4416  
A:Molecule type: protein  
A:Residues: 361-372; 390-399; 504-613; 632-639; 647-656; 699-729; 731-743; 761-781; 818-826 <KAN>  
A:Experimental source: erythrocyte  
A:Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823,  
R:Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.  
J. Biol. Chem. 269, 1918-1926, 1994  
A:Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4  
A:Reference number: A49717; MUID:94124538; PMID:8294441  
A:Accession: A49717  
A:Molecule type: protein  
A:Residues: 427-436; 479-519; 538-540; 559-566; 809-817; 825-841; 849-857 <OKU>  
A:Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport  
R:Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.  
J. Biochem. 122, 577-585, 1997  
A:Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel  
A:Reference number: PC4403; MUID:98006310; PMID:9348087  
A:Accession: PC4403  
A:Molecule type: protein  
A:Residues: 361-911 <HAM>  
A:Note: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dimer

C:Comment: Band 3 has at least two functional domains. Its integral domain mediates a  
ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.  
C:Genetics:  
A:Gene: GDB:SLC4A1; EPB3  
A:Cross-References: GDB:119874; OMIM:109270  
A:Map position: 17q21-17q22  
C:Superfamily: band 3 anion transport protein  
C:Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transmembrane  
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F:404-911/Region: anion antiporter  
F:405-421/Domain: transmembrane #status predicted <TM01>  
F:435-457/Domain: transmembrane #status predicted <TM02>  
F:459-479/Domain: transmembrane #status predicted <TM03>  
F:491-507/Domain: transmembrane #status predicted <TM04>  
F:522-542/Domain: transmembrane #status predicted <TM05>  
F:568-588/Domain: transmembrane #status predicted <TM06>  
F:604-624/Domain: transmembrane #status predicted <TM07>  
F:659-680/Domain: transmembrane #status predicted <TM08>  
F:701-721/Domain: transmembrane #status predicted <TM09>  
F:723-743/Domain: transmembrane #status predicted <TM10>  
F:764-780/Domain: transmembrane #status predicted <TM11>  
F:785-806/Domain: transmembrane #status predicted <TM12>  
F:839-859/Domain: transmembrane #status predicted <TM13>  
F:861-881/Domain: transmembrane #status predicted <TM14>  
F:1/Modified site: acetylated amino end (Met) #status experimental  
F:539,590,851/Binding site: anion (Lys) #status experimental  
F:642/Binding site: carbohydrate (Asn) (covalent) #status predicted  
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Best Local Similarity 100.0%; Pred. No. 5e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVTHANALTVMGKASTPGAA 20  
Db 731 SVTHANALTVMGKASTPGAA 750  
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RESULT 2  
A33810  
band 3 anion transport protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Aug-1999  
C:Accession: A33810  
R:Kudrycki, K.E.; Shull, G.E.  
J. Biol. Chem. 264, 8185-8192, 1989  
A:Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr  
A:Reference number: A33810; MUID:8925254; PMID:2722777  
A:Accession: A33810  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-848 <KUD>  
A:Cross-References: GB:J04793; MID:g203092; PIDN:AAA40800.1; PID:g203093  
C:Superfamily: band 3 anion transport protein  
C:Keywords: alternative splicing; transmembrane protein  
Query Match 92.9%; Score 91; DB 2; Length 848;  
Best Local Similarity 95.0%; Pred. No. 6.7e-07;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SVTHANALTVMGKASTPGAA 20  
Db 668 SVTHANALTVMGKASTPGAA 687  
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RESULT 3  
A25314  
band 3 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Aug-1999  
C:Accession: A25314; A26086; I49524; B25104  
R:Kopito, R.R.; Lodish, H.F.  
Nature 316, 234-238, 1985  
A:Title: Primary structure and transmembrane orientation of the murine anion exchange

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A:Reference number: A25314; MUID:85268011; PMID:2410791  
 A:Accession: A25314  
 A:Molecule type: mRNA  
 A:Residues: 1-929 <KOP>  
 A:Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898  
 R:Kopito, R.R.; Lodish, H.F.  
 J. Cell. Biochem. 29, 1-17, 1985  
 A:Title: Structure of the murine anion exchange protein.  
 A:Reference number: A26086; MUID:86034211; PMID:3840489  
 A:Accession: A26086  
 A:Molecule type: mRNA  
 A:Residues: 1-929 <K02>  
 A:Cross-references: GB:X29379; NID:g191741; PIDN:AAA37187.1; PID:g191742  
 R:Kopito, R.R.; Andersson, M.; Lodish, H.F.  
 J. Biol. Chem. 262, 8035-8040, 1987  
 A:Title: Structure and organization of the murine band 3 gene.  
 A:Reference number: I49524; MUID:87250387; PMID:3036795  
 A:Accession: I49524  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 4-707, 'X', 709-902 <RES>  
 A:Cross-references: GB:J02756; PIDN:AA37278.1; PID:g553874  
 R:Smith, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera  
 EMBO J. 5, 1205-1214, 1986  
 A:Title: Cloning and structural characterization of a human non-erythroid band 3-like pr  
 A:Reference number: A91039; MUID:86274622; PMID:3015590  
 A:Accession: B25104  
 A:Molecule type: mRNA  
 A:Residues: 11-466, 'S', 468-929 <DEM>  
 A:Cross-references: GB:X03917; NID:g53042; PIDN:CAA27555.1; PID:g53043  
 C:Genetics:  
 A:Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: transmembrane protein

Query Match 92.9%; Score 91; DB 2; Length 929;  
 Best Local Similarity 95.0%; Pred. No. 7.4e-07;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SVTHANALTYMGKASTPGAA 20  
 |||||  
 DB 749 SVTHANALTYMGKASGPAA 768

RESULT 4  
 A25104  
 band 3 protein, nonerythroid (NEB3) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
 A:Accession: A25104  
 R:Smith, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera  
 EMBO J. 5, 1205-1214, 1986  
 A:Title: Cloning and structural characterization of a human non-erythroid band 3-like pr  
 A:Reference number: A91039; MUID:86274622; PMID:3015590  
 A:Accession: A25104  
 A:Molecule type: mRNA  
 A:Residues: 1-865 <DEM>  
 A:Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: transmembrane protein

Query Match 74.5%; Score 73; DB 2; Length 865;  
 Best Local Similarity 83.3%; Pred. No. 0.00068;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 SVTHANALTYMGKASTPG 18  
 |||||  
 DB 685 SVTHANALTYMGKASVAPG 702

RESULT 5  
 A34911  
 band 3-related protein 2 - rat

C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999  
 C:Accession: A34911; A35770  
 R:Kudrycki, K.E.; Newman, P.R.; Shull, G.E.  
 J. Biol. Chem. 265, 462-471, 1990  
 A:Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are r  
 A:Reference number: A34911; MUID:90094439; PMID:2294114  
 A:Accession: A34911  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1234 <KUD>  
 A:Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091  
 R:Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Barton, R.; Lee, B.S.; Kopito, R.R.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990  
 A:Title: Functional expression and subcellular localization of an anion exchanger  
 A:Reference number: A35770; MUID:90319095; PMID:2371270  
 A:Accession: A35770  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptua  
 A:Molecule type: mRNA  
 A:Residues: 1-205, 'A', 207-924, 'PG', 927-1017, 'IV', 1020-1155, 'ID', 1158-1234 <LIN>  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: transmembrane protein

Query Match 74.5%; Score 73; DB 2; Length 1234;  
 Best Local Similarity 83.3%; Pred. No. 0.00099;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 SVTHANALTYMGKASTPG 18  
 |||||  
 DB 1054 SVTHANALTYMGKASVAPG 1071

RESULT 6  
 A31789  
 band 3-related protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 20-Aug-1999  
 C:Accession: A31789  
 R:Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.  
 J. Biol. Chem. 263, 17092-17099, 1988  
 A:Title: Cloning and characterization of a murine band 3-related cDNA from kidney e  
 A:Reference number: A31789; MUID:89034212; PMID:3182834  
 A:Accession: A31789  
 A:Molecule type: mRNA  
 A:Residues: 1-1237 <ALP>  
 A:Cross-references: GB:J04036; NID:g192132; PIDN:AAA65505.1; PID:g309114  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: transmembrane protein

Query Match 74.5%; Score 73; DB 2; Length 1237;  
 Best Local Similarity 83.3%; Pred. No. 0.00099;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 SVTHANALTYMGKASTPG 18  
 |||||  
 DB 1057 SVTHANALTYMGKASVAPG 1074

RESULT 7  
 A56764  
 band 3-related protein, ileum - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 08-Sep-1995 #sequence\_revision 08-Sep-1995 #text\_change 20-Aug-1999  
 C:Accession: A56764  
 R:Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.  
 Am. J. Physiol. 263, G345-G352, 1992  
 A:Title: CDNA cloning and localization of a band 3-related protein from ileum.  
 A:Reference number: A56764; MUID:93035730; PMID:1415547  
 A:Accession: A56764  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1237 <CHO>  
 A:Cross-references: GB:S45791; NID:g256659; PIDN:AAB23488.1; PID:g256660

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:41:03 ; Search time 17.25 Seconds  
(without alignments)  
111.500 Million cell updates/sec

Title: US-10-087-464-3  
Perfect score: 96  
Sequence: 1 GRASTPGAAQIQVEKQRI 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR76:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	911	1 B3HU	band 3 anion trans
2	89	92.7	848	2 A33810	band 3 anion trans
3	89	92.7	929	2 A25314	band 3 protein - m
4	61	63.5	844	2 I50159	anion transporter
5	61	63.5	922	2 A30816	band 3 anion trans
6	58	60.4	865	2 A25104	band 3 protein, no
7	58	60.4	1234	2 A34911	band 3-related pro
8	58	60.4	1237	2 A31789	band 3-related pro
9	58	60.4	1237	2 A56764	band 3-related pro
10	58	60.4	1240	2 S21086	anion exchange pro
11	54	56.2	357	2 S31828	band 3 anion trans
12	54	56.2	1030	2 A42497	band 3 anion trans
13	54	56.2	1227	2 B34911	anion exchanger 3,
14	54	56.2	1227	2 A33638	band 3-related pro
15	54	56.2	1232	2 I38496	erythrocyte anion
16	50	52.1	1317	2 T03748	anion exchanger 3
17	48	50.0	346	2 F75377	apoptosis associat
18	48	50.0	362	2 D82644	ABC transporter, A
19	45	46.9	329	2 E82644	sugar-phosphate de
20	45	46.9	391	1 RRN2YA	sugar-phosphate de
21	45	46.9	391	1 RRN2ED	polymerase-associa
22	45	46.9	826	2 T28858	polymerase-associa
23	44	45.8	391	2 T36321	hypothetical prote
24	44	45.8	455	2 J54722	hypothetical prote
25	44	45.8	459	2 I55472	nucleobindin precu
26	44	45.8	1369	2 D86178	Calcium binding pr
27	44	45.8	1495	2 T48429	hypothetical prote
28	43	44.8	324	2 F95386	hypothetical prote
29	43	44.8	416	2 D90938	protein [Imported probable transport

#### ALIGNMENTS

##### RESULT 1

B3HU band 3 anion transport protein, erythrocyte - human  
N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion exci  
C:Species: Homo sapiens (man)  
C>Date: 03-Aug-1984 #sequence\_revision 03-Oct-1995 #text\_change 22-Jun-1999  
C:Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079.  
R:Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989  
A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchang  
A:Reference number: A36218; MUID:90083213; PMID:2594752  
A:Accession: A36218  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-911 <LU>  
A:Cross-references: GB:M27819; NID:gl78215; PIDN:AAA35514.1; PID:gl78216  
R:Tanner, M.J.A.; Martin, P.G.; High, S.  
Biochem. J. 256, 703-712, 1988  
A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-t  
A:Reference number: S03074; MUID:89134172; PMID:3223947  
A:Accession: S03074  
A:Molecule type: mRNA  
A:Residues: 1-55, 'E', '57-911 <TAN>  
A:Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714  
R:Shove, L.C.; Ballantine, M.; Huebner, K.  
Genomics 1, 71-76, 1987  
A:Title: Localization of the gene for the erythroid anion exchange protein, band 3 (  
A:Reference number: I39408; MUID:88031311; PMID:3478298  
A:Accession: I39408  
A:Molecule type: DNA  
A:Residues: 37-56 <SHO1>  
A:Cross-references: GB:M16978; NID:gl78217; PIDN:AAA51670.1; PID:gl78220  
A:Accession: I39409  
A:Molecule type: DNA  
A:Residues: 118-161 <SHO2>  
A:Cross-references: GB:M16979; NID:gl78218; PIDN:AAA51671.1; PID:g553169  
R:Drickamer, L.K.  
J. Biol. Chem. 253, 7242-7248, 1978  
A:Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Ide  
A:Reference number: A92237; MUID:79027186; PMID:701248  
A:Accession: A92237  
A:Molecule type: protein  
A:Residues: 1-3 <DRI>  
R:Mawby, W.J.; Findlay, J.B.C.  
Biochem. J. 205, 465-475, 1982  
A:Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate  
A:Reference number: A26507; MUID:83074521; PMID:7150226  
A:Accession: A26507  
A:Molecule type: protein  
A:Residues: 437-473; 360-364, 'D', 366-369 <MAW>  
R:Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.  
J. Biol. Chem. 258, 7981-7990, 1983

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A:Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte  
A:Reference number: A92430; MUID:83238395; PMID:6345535  
A:Accession: A92430  
A:Molecule type: protein  
A:Residues: 1-10, 'D', 12-68, 'E', 69-200 <KAW>  
R:Brock, C.J.; Tanner, M.J.A.; Kempf, C.  
Biochem. J. 213, 577-586, 1983  
A:Title: The human erythrocyte anion-transport protein.  
A:Reference number: A90323; MUID:83308584; PMID:6615451  
A:Accession: A90323  
A:Molecule type: protein  
A:Residues: 559-630 <BRO>  
A:Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport  
R:Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.  
J. Biol. Chem. 263, 8232-8238, 1988  
A:Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal region  
A:Reference number: A28079; MUID:88228050; PMID:3372523  
A:Accession: A28079  
A:Molecule type: protein  
A:Residues: 834-842, 'X', 844-911 <KAW>  
A:Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate for  
R:Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajzman, H.  
Biochim. Biophys. Acta 998, 43-49, 1989  
A:Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3  
A:Reference number: S05523; MUID:90001294; PMID:2790053  
A:Accession: S05523  
A:Molecule type: protein  
A:Residues: 1-201; 220-292; 307-308, 'R', 310-312, 'S', 314-329, 'K', 331-333; 347-370 <YANI>  
R:Cobb, C.E.; Beth, A.H.  
Biochemistry 29, 8283-8290, 1990  
A:Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyte  
A:Reference number: A35835; MUID:91070049; PMID:1701324  
A:Accession: A35835  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 361-364, 'X', 366-372; 424-429, 'X', 431-434 <COB>  
A:Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes  
R:Yannoukakos, D.; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajzman, H.;  
Blood 78, 1117-1120, 1991  
A:Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the  
A:Reference number: A44933; MUID:91329825; PMID:1678289  
A:Accession: A44933  
A:Molecule type: protein  
A:Residues: 1-55, 'E', 57-69 <YAN2>  
A:Note: sequence extracted from NCBI backbone (NCBIP:49829)  
A:Note: sequence of a common polymorphic form designated band 3 Memphis  
R:Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.  
J. Biol. Chem. 267, 19211-19217, 1992  
A:Title: A structural study of the membrane domain of band 3 by tryptic digestion. Conf  
A:Reference number: A44116; MUID:92406862; PMID:1527044  
A:Accession: A44116  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 361-372; 390-399; 604-613; 632-639; 647-656; 699-729; 731-743; 761-781; 818-826 <KAN>  
A:Experimental source: erythrocyte  
A:Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823,  
A:Note: a histidine residue essential for anion transport is suggested to be His-651, H  
R:Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.  
J. Biol. Chem. 269, 1918-1926, 1994  
A:Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4  
A:Reference number: A49717; MUID:94124538; PMID:8294441  
A:Accession: A49717  
A:Molecule type: protein  
A:Residues: 427-436; 479-519; 538-540; 559-566; 809-817; 825-841; 849-857 <OKU>  
A:Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport  
R:Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.  
J. Biochem. 122, 577-585, 1997  
A:Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fide  
A:Reference number: PC4403; MUID:98006310; PMID:9348087  
A:Accession: PC4403  
A:Molecule type: protein  
A:Residues: 361-911 <HAM>  
A:Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime

C:Comment: Band 3 has at least two functional domains. Its integral domain mediates a  
ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.  
C:Genetics:  
A:Gene: GDB:SLC4A1; EPB3  
A:Cross-references: GDB:119874; OMIM:109270  
A:Map position: 17q21-17q22  
C:Superfamily: band 3 anion transport protein  
C:Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm  
F:1-403/Region: cytoskeletal protein binding  
F:404-911/Region: anion antiporter  
F:405-421/Domain: transmembrane #status predicted <TM01>  
F:435-457/Domain: transmembrane #status predicted <TM02>  
F:459-479/Domain: transmembrane #status predicted <TM03>  
F:491-507/Domain: transmembrane #status predicted <TM04>  
F:522-542/Domain: transmembrane #status predicted <TM05>  
F:568-588/Domain: transmembrane #status predicted <TM06>  
F:604-624/Domain: transmembrane #status predicted <TM07>  
F:659-680/Domain: transmembrane #status predicted <TM08>  
F:701-721/Domain: transmembrane #status predicted <TM09>  
F:723-743/Domain: transmembrane #status predicted <TM10>  
F:764-780/Domain: transmembrane #status predicted <TM11>  
F:785-806/Domain: transmembrane #status predicted <TM12>  
F:839-859/Domain: transmembrane #status predicted <TM13>  
F:861-881/Domain: transmembrane #status predicted <TM14>  
F:1/Modified site: acetylated amino end (Met) #status experimental  
F:539,590,851/Binding site: anion (Lys) #status experimental  
F:642/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 96; DB 1; Length 911;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAAIQIEVKEQRI 20  
|||||  
Db 742 GRASIPGAAAIQIEVKEQRI 761

RESULT 2  
A33810  
band 3 anion transport protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Aug-1999  
R:Kudrycki, K.E.; Shull, G.E.  
J. Biol. Chem. 264, 8185-8192, 1989  
A:Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr  
A:Reference number: A33810; MUID:89255254; PMID:2722777  
A:Accession: A33810  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-848 <KUD>  
A:Cross-references: GB:J04793; NID:g203092; PIDN:AAAA0800.1; PID:g203093  
A:Superfamily: band 3 anion transport protein  
C:Keywords: alternative splicing; transmembrane protein

Query Match 92.7%; Score 89; DB 2; Length 848;  
Best Local Similarity 95.0%; Pred. No. 1.2e-05;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKASTPGAAAIQIEVKEQRI 20  
|||||  
Db 679 GRASIPGAAAIQIEVKEQRI 698

RESULT 3  
A25314  
band 3 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Aug-1999  
A:Accession: A25314; A26086; I49524; B25104  
R:Kopito, R.R.; Lodish, H.F.  
Nature 316, 234-238, 1985  
A:Title: Primary structure and transmembrane orientation of the murine anion exchange

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A:Reference number: A25314; MUID:85268011; PMID:2410791  
A:Accession: A25314  
A:Molecule type: mRNA  
A:Residues: 1-929 <KOP>  
A:Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898  
R:Kopito, R.R.; Lodish, H.F.  
J. Cell. Biochem. 29, 1-17, 1985  
A:Title: Structure of the murine anion exchange protein.  
A:Reference number: A26086; MUID:86034211; PMID:3840489  
A:Accession: A26086  
A:Molecule type: mRNA  
A:Residues: 1-929 <KO>  
A:Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742  
R:Kopito, R.R.; Andersson, M.; Lodish, H.F.  
J. Biol. Chem. 262, 8035-8040, 1987  
A:Title: Structure and organization of the murine band 3 gene.  
A:Reference number: I49524; MUID:87250387; PMID:3036795  
A:Accession: I49524  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 4-707, 'X', 709-902 <RES>  
A:Cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874  
R:Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera  
EMBO J. 5, 1205-1214, 1986  
A:Title: Cloning and structural characterization of a human non-erythroid band 3-like pr  
A:Reference number: A91039; MUID:86274622; PMID:3015590  
A:Accession: B25104  
A:Molecule type: mRNA  
A:Residues: 11-466, 'S', 468-929 <DEM>  
A:Cross-references: GB:X03917; NID:g53042; PIDN:CAA27555.1; PID:g53043  
C:Genetics:  
A:Insertions: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/  
A:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein  
Query Match 92.7%; Score 89; DB 2; Length 929;  
Best Local Similarity 95.0%; Pred. No. 1.3e-05;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GRASPGGAAAIQIEVKQRI 20  
Db 760 GRASPGGAAAIQIEVKQRI 779  
RESULT 4  
50159  
anion transporter - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 20-Aug-1999  
C:Accession: I50159  
R:Cox, J.V.; Lazarides, E.  
Mol. Cell. Biol. 8, 1327-1335, 1988  
A:Title: Alternative primary structures in the transmembrane domain of the chicken eryth  
A:Reference number: I50159; MUID:88216609; PMID:2835670  
A:Accession: I50159  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-844 <COX>  
A:Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212  
C:Superfamily: band 3 anion transport protein  
Query Match 63.5%; Score 61; DB 2; Length 844;  
Best Local Similarity 60.0%; Pred. No. 0.25;  
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GKASTPGAAAIQIEVKQRI 20  
Db 675 GKSAVPGERAHIVEVKQRL 694  
RESULT 5  
A30816  
band 3 anion transport protein (clone pBIIIC1) - chicken

C:Species: Gallus gallus (chicken)  
C:Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 16-Feb-1997  
C:Accession: A30816  
R:Kim, H.R.C.; Yew, N.S.; Ansoorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke,  
Mol. Cell. Biol. 8, 4416-4424, 1988  
A:Title: Two different mRNAs are transcribed from a single genomic locus encoding the  
A:Reference number: A30816; MUID:89039870; PMID:3185555  
A:Accession: A30816  
A:Molecule type: mRNA  
A:Residues: 1-922 <KIM>  
A:Cross-references: GB:M23404  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein  
Query Match 63.5%; Score 61; DB 2; Length 922;  
Best Local Similarity 60.0%; Pred. No. 0.27;  
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GKASTPGAAAIQIEVKQRI 20  
Db 753 GKSAVPGERAHIVEVKQRL 772  
RESULT 6  
A25104  
band 3 protein, nonerythroid (MEB3) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C:Accession: A25104  
R:Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rov  
EMBO J. 5, 1205-1214, 1986  
A:Title: Cloning and structural characterization of a human non-erythroid band 3-like  
A:Reference number: A91039; MUID:86274622; PMID:3015590  
A:Accession: A25104  
A:Molecule type: mRNA  
A:Residues: 1-865 <DEM>  
A:Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein  
Query Match 60.4%; Score 58; DB 2; Length 865;  
Best Local Similarity 63.2%; Pred. No. 0.73;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 2 KASTPGAAAIQIEVKQRI 20  
Db 697 KAVAPGDKPKIIEVKQRV 715  
RESULT 7  
A34911  
band 3-related protein 2 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999  
C:Accession: A34911; A35770  
R:Kudrycki, K.E.; Newman, P.R.; Shull, G.E.  
J. Biol. Chem. 265, 462-471, 1990  
A:Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are rel  
A:Reference number: A34911; MUID:90094439; PMID:2294114  
A:Accession: A34911  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1234 <KUD>  
A:Cross-references: GB:J03166; NID:g203090; PIDN:AAA40799.1; PID:g203091  
R:Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990  
A:Title: Functional expression and subcellular localization of an anion exchanger cl  
A:Reference number: A35770; MUID:90319095; PMID:2371270  
A:Accession: A35770  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
A:Molecule type: mRNA  
A:Residues: 1-205, 'A', 207-924, 'PG', 927-1017, 'IV', 1020-1155, 'ID', 1158-1234 <LIN>  
C:Superfamily: band 3 anion transport protein

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OM protein - protein search, using sw model  
Run on: September 3, 2003, 11:41:03 : Search time 17.25 seconds  
(without alignments)  
111.500 Million cell updates/sec

Title: US-10-087-464-4  
Perfect score: 112  
Sequence: 1 DRILLFRPKVHPDVPYVK 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	911	1 B3HU	band 3 anion trans
2	108	96.4	848	2 A33810	band 3 anion trans
3	108	96.4	929	2 A25314	band 3 protein - m
4	82	73.2	844	2 A50159	anion transporter
5	82	73.2	922	2 A30816	band 3 anion trans
6	74	66.1	865	2 A25104	band 3 protein, no
7	74	66.1	1234	2 A34911	band 3-related pro
8	74	66.1	1237	2 A31789	band 3-related pro
9	74	66.1	1237	2 A56764	band 3-related pro
10	74	66.1	1240	2 S21086	anion exchange pro
11	68	60.7	1030	2 A42497	anion exchanger 3,
12	68	60.7	1227	2 B34911	erythrocyte anion
13	68	60.7	1227	2 A33638	probable sodium bi
14	66	58.9	1119	2 T37460	hypothetical prote
15	66	58.9	1175	2 T22491	sodium bicarbonate
16	63	56.2	1035	2 T31336	anion exchanger 3
17	62	55.4	1232	2 T38496	acid phosphatase (
18	50	44.6	468	1 B84540	band 3 anion trans
19	50	44.6	912	2 S9861	band 3 anion trans
20	50	44.6	918	2 S24318	BGLF2 protein - hu
21	49	43.8	336	1 Q0BE40	acid phosphatase (
22	49	43.8	469	1 H84669	acid phosphatase (
23	49	43.8	473	1 A59200	Na+ bicarbonate co
24	49	43.8	1079	2 PC7034	probable histone d
25	48	42.9	334	2 B5095	hypothetical prote
26	48	42.9	335	1 H71071	methyiaspartate am
27	48	42.9	413	2 T43810	sporulation specif
28	48	42.9	605	2 C96940	sodium bicarbonate
29	48	42.9	1035	2 T13962	

30 48 42.9 1035 2 T14110 sodium bicarbonate  
31 48 42.9 1079 2 T14031 sodium bicarbonate  
32 47 42.0 234 2 F69019 conserved hypothet  
33 47 42.0 284 2 B84146 transglutaminase t  
34 47 42.0 466 1 T04599 acid phosphatase (t  
35 47 42.0 466 1 F96605 acid phosphatase (t  
36 46 41.1 137 2 T30143 hypothetical prote  
37 46 41.1 306 2 E72237 hypothetical prote  
38 46 41.1 468 2 G82329 hypothetical prote  
39 46 41.1 1156 2 T23748 hypothetical prote  
40 45 40.6 77 2 AH1642 alpha 2,6-sialyltr  
41 45 40.2 214 2 C42327 beta-galactoside a  
42 45 40.2 403 2 A28451 beta-galactoside a  
43 45 40.2 406 2 A41734 acid phosphatase (t  
44 45 40.2 431 1 A59201 acid phosphatase (t  
45 45 40.2 434 2 S11967 nodule-specific hy

ALIGNMENTS

RESULT 1  
B3HU  
band 3 anion transport protein, erythrocyte - human  
N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha  
C:Species: Homo sapiens (man)  
C:Date: 03-Aug-1984 #sequence\_revision 03-Oct-1995 #text\_change 22-Jun-1999  
C:Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079;  
R:Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989  
A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange  
A:Reference number: A36218; MUID:90083213; PMID:2594752  
A:Accession: A36218  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-911 <LUX>  
A:Cross-references: GB:M27819; NID:g178215; PIDN:AAA35514.1; PID:g178216  
R:Tanner, M.J.A.; Martin, P.G.; High, S.  
Biochem. J. 256, 703-712, 1988  
A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-tr  
A:Reference number: S03074; MUID:89134172; PMID:3223947  
A:Accession: S03074  
A:Molecule type: mRNA  
A:Residues: 1-55, 'E', '57-911 <TAN>  
A:Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714  
R:Shove, L.C.; Ballantine, M.; Huebner, K.  
Genomics 1, 71-76, 1987  
A:Title: Localization of the gene for the erythroid anion exchange protein, band 3 (t  
A:Reference number: I39408; MUID:88031311; PMID:3478298  
A:Accession: I39408  
A:Molecule type: DNA  
A:Residues: 37-56 <SHOL>  
A:Cross-references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220  
A:Accession: I39409  
A:Molecule type: DNA  
A:Residues: 118-161 <SHO2>  
A:Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g553169  
R:Drickamer, L.K.  
J. Biol. Chem. 253, 7242-7248, 1978  
A:Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Ide  
A:Reference number: A92237; MUID:79027186; PMID:701248  
A:Accession: A92237  
A:Molecule type: protein  
A:Residues: 1-3 <DRI>  
R:Mayby, W.J.; Findlay, J.B.C.  
Biochem. J. 205, 465-475, 1982  
A:Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate  
A:Reference number: A26507; MUID:83074521; PMID:7150226  
A:Accession: A26507  
A:Molecule type: protein  
A:Residues: 437-473;360-364, 'D', '366-369 <MAW>  
R:Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.  
J. Biol. Chem. 258, 7981-7990, 1983

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A:Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte  
 A:Reference number: A92430; MUID:83238395; PMID:6345535  
 A:Accession: A92430  
 A:Molecule type: protein  
 A:Residues: 1-10,'D',12-68,'E',69-200 <KAU>  
 R:Brook, C.J.; Tanner, M.J.A.; Kempf, C.  
 Biochem. J. 213, 577-586, 1983  
 A:Title: The human erythrocyte anion-transport protein.  
 A:Reference number: A90323; MUID:83308584; PMID:6615451  
 A:Accession: A90323  
 A:Molecule type: protein  
 A:Residues: 559-630 <BRO>  
 A:Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport  
 R:Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.  
 J. Biol. Chem. 263, 8232-8238, 1988  
 A:Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal region  
 A:Reference number: A28079; MUID:88228050; PMID:3372523  
 A:Accession: A28079  
 A:Molecule type: protein  
 A:Residues: 834-842,'X',844-911 <KAW>  
 A:Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate for  
 R:Panoukakis, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.  
 Biochim. Biophys. Acta 998, 43-49, 1989  
 A:Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3  
 A:Reference number: S05523; MUID:90001294; PMID:2790053  
 A:Accession: S05523  
 A:Molecule type: protein  
 A:Residues: 1-201;220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 <YAN1>  
 R:Cobb, C.E.; Beth, A.H.  
 Biochemistry 29, 8283-8290, 1990  
 A:Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyte  
 A:Reference number: A35835; MUID:91070049; PMID:1701324  
 A:Accession: A35835  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 361-364,'X',366-372;424-429,'X',431-434 <COB>  
 A:Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes  
 R:Rannoukakis, D.; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.;  
 Blood 78, 1117-1120, 1991  
 A:Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the  
 A:Reference number: A44933; MUID:91329825; PMID:1678289  
 A:Accession: A44933  
 A:Molecule type: protein  
 A:Residues: 1-55,'E',57-69 <YAN2>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:49829)  
 A:Note: sequence of a common polymorphic form designated band 3 Memphis  
 R:Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.  
 J. Biol. Chem. 267, 19211-19217, 1992  
 A:Title: A structural study of the membrane domain of band 3 by tryptic digestion. Conf  
 A:Reference number: A44116; MUID:92408662; PMID:1527044  
 A:Accession: A44116  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <KAN>  
 A:Experimental source: erythrocyte  
 A:Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113823,  
 R:Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.  
 J. Biol. Chem. 269, 1918-1926, 1994  
 A:Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4  
 A:Reference number: A49717; MUID:94124538; PMID:8294441  
 A:Accession: A49717  
 A:Molecule type: protein  
 A:Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>  
 A:Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport  
 R:Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.  
 J. Biochem. 122, 577-585, 1997  
 A:Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel  
 A:Reference number: PC4403; MUID:98006310; PMID:9348087  
 A:Accession: PC4403  
 A:Molecule type: protein  
 A:Residues: 361-911 <HAM>  
 A:Note: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime

C:Comment: Band 3 has at least two functional domains. Its integral domain mediates a  
 ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.

C:Genetics:  
 A:Gene: GDB:SLC4A1; EPB3  
 A:Cross-references: GDB:119874; OMIM:109270  
 A:Map position: 17q21-17q22  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; trans  
 F:1-403/Region: cytoskeletal protein binding  
 F:404-911/Region: anion antiporter  
 F:405-427/Domain: transmembrane #status predicted <TM01>  
 F:435-457/Domain: transmembrane #status predicted <TM02>  
 F:459-479/Domain: transmembrane #status predicted <TM03>  
 F:491-507/Domain: transmembrane #status predicted <TM04>  
 F:522-542/Domain: transmembrane #status predicted <TM05>  
 F:568-588/Domain: transmembrane #status predicted <TM06>  
 F:604-624/Domain: transmembrane #status predicted <TM07>  
 F:659-680/Domain: transmembrane #status predicted <TM08>  
 F:701-721/Domain: transmembrane #status predicted <TM09>  
 F:723-743/Domain: transmembrane #status predicted <TM10>  
 F:764-780/Domain: transmembrane #status predicted <TM11>  
 F:785-806/Domain: transmembrane #status predicted <TM12>  
 F:839-859/Domain: transmembrane #status predicted <TM13>  
 F:861-881/Domain: transmembrane #status predicted <TM14>  
 F:1/Modified site: acetylated amino end (Met) #status experimental  
 F:539,590,851/Binding site: anion (Lys) #status experimental  
 F:642/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 112; DB 1; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFPKPKYHPDVPYVK 20  
 DB 807 DRILLFPKPKYHPDVPYVK 826

## RESULT 2

A33810  
 band 3 anion transport protein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Aug-1999  
 C:Accession: A33810  
 R:Kudrycki, K.E.; Shull, G.E.  
 J. Biol. Chem. 264, 8185-8192, 1989  
 A:Title: Primary structure of the rat kidney band 3 anion exchange protein deduced f  
 A:Reference number: A33810; MUID:89255254; PMID:2722777  
 A:Accession: A33810  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-848 <KUD>  
 A:Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: alternative splicing; transmembrane protein

Query Match 96.4%; Score 108; DB 2; Length 848;  
 Best Local Similarity 95.0%; Pred. No. 2.1e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFPKPKYHPDVPYVK 20  
 DB 744 DRILLFPKPKYHPDVPYVK 763

## RESULT 3

A25314  
 band 3 protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Aug-1999  
 C:Accession: A25314; A26086; I49524; B25104  
 R:Kopito, R.R.; Lodish, H.F.  
 Nature 316, 234-238, 1985  
 A:Title: Primary structure and transmembrane orientation of the murine anion exchange

3 19.

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C:Species: Gallus gallus (chicken)  
C:Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 16-Feb-1997  
C:Accession: A30816  
R:Kim, H.R.C.; Voss, H.; Schwager, C.; Vennstrom, B.; Zenke, M.; Cell. Biol. 8, 4416-4424, 1988  
A:Title: Two different mRNAs are transcribed from a single genomic locus encoding the anion exchanger c1  
A:Reference number: A30816; MUID:89039870; PMID:3185555  
A:Accession: A30816  
A:Molecule type: mRNA  
A:Residues: 1-922 <KIM>  
A:Cross-references: GB:M23404  
A:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

Query Match 73.2%; Score 82; DB 2; Length 922;  
Best Local Similarity 78.9%; Pred. No. 0.00022;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRILLFKPKYHPDVPYV 19  
Db 818 DRILLMLPPKYHPKPEYV 836

RESULT 6  
A25104  
band 3 protein, nonerythroid (MEB3) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C:Accession: A25104  
R:Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Ro-  
EMBO J. 5, 1205-1214, 1986  
A:Title: Cloning and structural characterization of a human non-erythroid band 3-like  
A:Reference number: A91039; MUID:86274622; PMID:3015590  
A:Accession: A25104  
A:Molecule type: mRNA  
A:Residues: 1-865 <DEM>  
A:Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121  
A:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

Query Match 66.1%; Score 74; DB 2; Length 865;  
Best Local Similarity 65.0%; Pred. No. 0.0034;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRILLFKPKYHPDVPYV 20  
Db 761 ERLHLLMPPKHPDVPYV 780

RESULT 7  
A34911  
band 3-related protein 2 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999  
C:Accession: A34911; A35770  
R:Kudrycki, K.E.; Newman, P.R.; Shull, G.E.  
J. Biol. Chem. 265, 462-471, 1990  
A:Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are rel  
A:Reference number: A34911; MUID:90094439; PMID:2294114  
A:Accession: A34911  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1234 <KUD>  
A:Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091  
R:Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990  
A:Title: Functional expression and subcellular localization of an anion exchanger c1  
A:Reference number: A35770; MUID:90319095; PMID:2371270  
A:Accession: A35770  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptua.  
A:Molecule type: mRNA  
A:Residues: 1-205, 'A', 207-924, 'PG', 927-1017, 'IV', 1020-1155, 'ID', 1158-1234 <LIN>  
C:Superfamily: band 3 anion transport protein

A:Reference number: A25314; MUID:85268011; PMID:2410791  
A:Accession: A25314  
A:Molecule type: mRNA  
A:Residues: 1-929 <KOP>  
A:Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898  
R:Kopito, R.R.; Lodish, H.F.  
J. Cell. Biochem. 29, 1-17, 1985  
A:Title: Structure of the murine anion exchange protein.  
A:Reference number: A26086; MUID:86034211; PMID:3840489  
A:Accession: A26086  
A:Molecule type: mRNA  
A:Residues: 1-929 <KOP>  
A:Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742  
R:Kopito, R.R.; Andersson, M.; Lodish, H.F.  
J. Biol. Chem. 262, 8035-8040, 1987  
A:Title: Structure and organization of the murine band 3 gene.  
A:Reference number: I49524; MUID:87250387; PMID:3036795  
A:Accession: I49524  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 4-707, 'X', 709-902 <RES>  
A:Cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874  
R:Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera  
EMBO J. 5, 1205-1214, 1986  
A:Title: Cloning and structural characterization of a human non-erythroid band 3-like pr  
A:Reference number: A91039; MUID:86274622; PMID:3015590  
A:Accession: B25104  
A:Molecule type: mRNA  
A:Residues: 11-466, 'S', 468-929 <DEM>  
A:Cross-references: GB:X03917; NID:g53042; PIDN:CAA27555.1; PID:g53043  
C:Genetics:  
A:Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/  
A:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

Query Match 96.4%; Score 108; DB 2; Length 929;  
Best Local Similarity 95.0%; Pred. No. 2.3e-08;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRILLFKPKYHPDVPYV 20  
Db 825 DRILLFKPKYHPDVPYV 844

RESULT 4  
I50159  
anion transporter - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 20-Aug-1999  
C:Accession: I50159  
R:Cox, J.V.; Lazarides, E.  
Mol. Cell. Biol. 8, 1327-1335, 1988  
A:Title: Alternative primary structures in the transmembrane domain of the chicken eryth  
A:Reference number: I50159; MUID:88216609; PMID:2835670  
A:Accession: I50159  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-844 <COX>  
A:Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212  
C:Superfamily: band 3 anion transport protein

Query Match 73.2%; Score 82; DB 2; Length 844;  
Best Local Similarity 78.9%; Pred. No. 0.0002; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRILLFKPKYHPDVPYV 19  
Db 740 DRILLMLPPKYHPKPEYV 758

RESULT 5  
A30816  
band 3 anion transport protein (clone pBIIIC1) - chicken

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:46:23 ; Search time 17.5 Seconds  
(without alignments)  
156.918 Million cell updates/sec

Title: US-10-087-464-1

Perfect score: 104

Sequence: 1 GMPWLSATTVRSVTHANALT 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	104	100.0	42	15	US-10-087-464-22
3	104	100.0	86	9	US-09-864-761-39328
4	104	100.0	911	15	US-10-066-320-2
5	104	100.0	911	15	US-10-087-464-6
6	104	100.0	911	15	US-10-087-464-8
7	66	63.5	714	9	US-09-728-137-4
8	66	63.5	1032	9	US-09-728-137-8
9	66	63.5	1044	9	US-09-728-137-2
10	66	63.5	1085	9	US-09-734-674-4
11	66	63.5	1085	15	US-10-274-990-4
12	66	63.5	1088	9	US-09-920-804-2
13	66	63.5	1088	9	US-09-920-804-4
14	66	63.5	1129	9	US-09-734-674-2
15	66	63.5	1129	15	US-10-274-990-2

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17	47	45.2	1035	15	US-10-205-823-373	Sequence 373, App
18	44.5	42.8	217	9	US-09-811-284-177	Sequence 177, App
19	44	42.3	20	15	US-10-087-464-2	Sequence 2, Appli
20	44	42.3	633	14	US-10-001-852-5	Sequence 5, Appli
21	44	42.3	875	14	US-10-001-852-2	Sequence 2, Appli
22	44	42.3	891	14	US-10-001-852-6	Sequence 6, Appli
23	44	42.3	918	14	US-10-001-852-7	Sequence 7, Appli
24	43	41.3	88	10	US-09-880-503-1	Sequence 1, Appli
25	43	41.3	96	10	US-09-880-503-9	Sequence 9, Appli
26	43	41.3	135	10	US-09-880-503-4	Sequence 4, Appli
27	43	41.3	138	10	US-09-884-186-12	Sequence 12, Appli
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29	43	41.3	138	15	US-10-237-708-12	Sequence 12, Appli
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34	43	41.3	337	15	US-10-106-698-6266	Sequence 6266, Ap
35	43	41.3	403	10	US-09-880-503-6	Sequence 6, Appli
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38	43	41.3	431	12	US-10-301-822-161	Sequence 161, App
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42	43	41.3	696	15	US-10-156-761-10360	Sequence 10360, A
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44	43	41.3	3170	15	US-10-128-714-8504	Sequence 8504, Ap
45	42	40.4	589	14	US-10-108-605-355	Sequence 355, App

#### ALIGNMENTS

#### RESULT 1

US-10-087-464-1  
; Sequence 1, Application US/10087464  
; Publication No. US20030059436A1  
; GENERAL INFORMATION:  
; APPLICANT: Chishti, Athar  
; APPLICANT: Oh, Steven  
; APPLICANT: Liu, David  
; APPLICANT: Goel, Vikas  
; APPLICANT: Li, Xuerong  
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There  
; FILE REFERENCE: S1237/7019  
; CURRENT APPLICATION NUMBER: US/10/087,464  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-087-464-1

Query Match 100.0%; Score 104; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.2e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
DB 1 GMPWLSATTVRSVTHANALT 20

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US-10-087-464-22  
; Sequence 22, Application US/10087464  
; Publication No. US20030059436A1  
; GENERAL INFORMATION:

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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39328
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
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; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
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; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
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US-09-864-761-39328

Query Match 100.0%; Score 104; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
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DB 34 GMPWLSATTVRSVTHANALT 53

RESULT 4
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; Sequence 2, Application US/10066320
; Publication NO. US20030022267A1
; GENERAL INFORMATION:
; APPLICANT: Stamler, Jonathan S.
; APPLICANT: Gow, Andrew J.
; APPLICANT: Singel, David J.
; TITLE OF INVENTION: Method for Determining Physiological
; TITLE OF INVENTION: Effects of Hemoglobin
; FILE REFERENCE: 1818.1030-003
; CURRENT APPLICATION NUMBER: US/10/066,320
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US00/21101
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US60/146,680
; PRIOR FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-320-2

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DB 720 GMPWLSATTVRSVTHANALT 739

RESULT 5
US-10-087-464-6
; Sequence 6, Application US/10087464
; Publication NO. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar

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; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
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; ORGANISM: Homo sapiens
US-10-087-464-6

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GMPWLSATTVRSVTHANALT 20
Db      720 GMPWLSATTVRSVTHANALT 739
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RESULT 6
US-10-087-464-8
; Sequence 8, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
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; ORGANISM: Homo sapiens
US-10-087-464-8

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Db      720 GMPWLSATTVRSVTHANALT 739
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US-09-728-137-4
; Sequence 4, Application US/09728137
; Patent No. US20010029031A1
; GENERAL INFORMATION:
; APPLICANT: Walter F. Boron
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Nassirah Khandoudi
; APPLICANT: Xavier Martin
; APPLICANT: Steven Charles Jupe
; APPLICANT: Christopher John Rawlings
; APPLICANT: Trudy Rachel Doe
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30409-D1
; CURRENT APPLICATION NUMBER: US/09/728,137
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/115,954
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 97401714.7
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 97401713.9
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 98400272.5
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: EP 98400454.9
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-728-137-8

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; FILE REFERENCE: GH-30409-D1
; CURRENT APPLICATION NUMBER: US/09/728,137
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/115,954
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EP 97401714.7
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 97401713.9
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; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: EP 98400454.9
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 714
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-728-137-4

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Best Local Similarity 57.9%; Pred. No. 0.056;
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Db      509 GLPWFVAATVLSITHVNSL 527
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RESULT 8
US-09-728-137-8
; Sequence 8, Application US/09728137
; Patent No. US20010029031A1
; GENERAL INFORMATION:
; APPLICANT: Walter F. Boron
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Nassirah Khandoudi
; APPLICANT: Xavier Martin
; APPLICANT: Steven Charles Jupe
; APPLICANT: Christopher John Rawlings
; APPLICANT: Trudy Rachel Doe
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30409-D1
; CURRENT APPLICATION NUMBER: US/09/728,137
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/115,954
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EP 97401714.7
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 97401713.9
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 98400272.5
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: EP 98400454.9
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-728-137-8

Query Match      63.5%; Score 66; DB 9; Length 1032;
Best Local Similarity 57.9%; Pred. No. 0.081;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 GMPWLSATTVRSVTHANAL 19
Db      827 GLPWFVAATVLSITHVNSL 845
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## RESULT 11



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Job time : 17.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:42:58 ; Search time 15.75 Seconds  
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Perfect score: 104  
Sequence: 1 GMPWLSATTVRSVTHANAL 20

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Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	66	63.5	1129	4 US-09-734-674-2	Sequence 2, Appli
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7	43	41.3	89	4 US-09-101-272G-62	Sequence 62, Appl
8	43	41.3	138	2 US-08-797-689-12	Sequence 12, Appl
9	43	41.3	194	4 US-09-101-272G-80	Sequence 80, Appl
10	43	41.3	200	4 US-09-101-272G-73	Sequence 73, Appl
11	43	41.3	201	4 US-09-101-272G-96	Sequence 96, Appl
12	43	41.3	208	4 US-09-101-272G-98	Sequence 98, Appl
13	43	41.3	360	1 US-08-597-236-11	Sequence 11, Appl
14	43	41.3	360	1 US-08-746-682A-11	Sequence 11, Appl
15	43	41.3	365	1 US-08-093-741-83	Sequence 83, Appl
16	43	41.3	365	1 US-08-720-012-83	Sequence 83, Appl
17	43	41.3	393	2 US-08-560-098A-44	Sequence 44, Appl
18	43	41.3	393	3 US-08-967-024C-24	Sequence 24, Appl
19	43	41.3	393	3 US-08-967-024C-25	Sequence 25, Appl
20	43	41.3	411	1 US-08-087-163-1	Sequence 1, Appli
21	43	41.3	411	1 US-08-286-748B-18	Sequence 18, Appl
22	43	41.3	411	1 US-08-153-799-18	Sequence 18, Appl
23	43	41.3	411	2 US-08-560-098A-48	Sequence 48, Appl
24	43	41.3	411	3 US-09-181-816-1	Sequence 1, Appli
25	43	41.3	430	1 US-07-942-157A-3	Sequence 3, Appli
26	43	41.3	430	6 5219569-2	Patent No. 5219569
27	43	41.3	431	4 US-09-101-272G-1	Sequence 1, Appli

28	43	41.3	431	6 5188829-1	Patent No. 5188829
29	43	41.3	432	2 US-08-560-098A-47	Sequence 47, Appl
30	42	40.4	366	4 US-09-252-991A-27453	Sequence 27453, A
31	41	39.4	416	4 US-09-252-991A-24117	Sequence 24117, A
32	41	39.4	719	1 US-07-943-843-4	Sequence 4, Appli
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34	41	39.4	727	4 US-09-252-991A-26100	Sequence 26100, A
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36	40	38.5	111	4 US-09-252-991A-17821	Sequence 17821, A
37	40	38.5	588	2 US-08-459-346-12	Sequence 12, Appl
38	40	38.5	588	3 US-08-889-419-12	Sequence 12, Appl
39	40	38.5	588	4 US-08-402-542-12	Sequence 12, Appl
40	40	38.5	588	5 PCT-US93-07189-12	Sequence 12, Appl
41	39.5	38.0	484	4 US-09-266-965-17	Sequence 17, Appl
42	39	37.5	76	4 US-09-107-532A-3890	Sequence 3890, Ap
43	39	37.5	81	4 US-09-205-258-740	Sequence 740, App
44	39	37.5	89	4 US-09-252-991A-28044	Sequence 28044, A
45	39	37.5	114	4 US-09-205-258-739	Sequence 739, App

ALIGNMENTS

RESULT 1				
US-09-115-954-4				
; Sequence 4, Application US/09115954B				
; Patent No. 6200776				
; GENERAL INFORMATION:				
; APPLICANT: Boron, Walter F				
; APPLICANT: Brill, Antoine M				
; APPLICANT: Khandoudi, Nassirah				
; APPLICANT: Martin, Xavier				
; APPLICANT: Jupe, Steven C				
; APPLICANT: Rawlings, Christopher J				
; APPLICANT: Doe, Trudy R				
; TITLE OF INVENTION: NOVEL COMPOUNDS				
; FILE REFERENCE: GH-30409				
; CURRENT APPLICATION NUMBER: US/09/115,954B				
; CURRENT FILING DATE: 1998-07-15				
; EARLIER APPLICATION NUMBER: EP97401714.7				
; EARLIER FILING DATE: 1997-07-16				
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; SOFTWARE: Patentin Ver. 2.0				
; SEQ ID NO 4				
; LENGTH: 714				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
US-09-115-954-4				
Query Match 63.5%; Score 66; DB 3; Length 714;				
Best Local Similarity 57.9%; Pred. No. 0.032;				
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;				
QY 1 GMPWLSATTVRSVTHANAL 19				
:				
Db 509 GLPWFVAATVLSITHVNSL 527				
RESULT 2				
US-09-115-954-8				
; Sequence 8, Application US/09115954B				
; Patent No. 6200776				
; GENERAL INFORMATION:				
; APPLICANT: Boron, Walter F				
; APPLICANT: Brill, Antoine M				
; APPLICANT: Khandoudi, Nassirah				
; APPLICANT: Martin, Xavier				
; APPLICANT: Jupe, Steven C				
; APPLICANT: Rawlings, Christopher J				
; APPLICANT: Doe, Trudy R				
; TITLE OF INVENTION: NOVEL COMPOUNDS				
; FILE REFERENCE: GH-30409				
; CURRENT APPLICATION NUMBER: US/09/115,954B				

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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1085
; TYPE: PRT
; ORGANISM: Mus musculus

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## RESULT 7

US-09-101-272G-62  
; Sequence 62, Application US/09101272G  
; Patent No. 6509445  
; GENERAL INFORMATION:  
; APPLICANT: Nissin Food Products Co., Ltd.  
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR  
; FILE REFERENCE: Q50979  
; CURRENT APPLICATION NUMBER: US/09/101.272G  
; CURRENT FILING DATE: 1998-07-08  
; PRIOR APPLICATION NUMBER: JP 1059/1996  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 62  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: residues 43-131 of the ATF domain of uPA  
US-09-101-272G-62

Query Match 41.3%; Score 43; DB 4; Length 89;  
Best Local Similarity 43.8%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MPWLSATVRSVTHAN 17  
: || ||| : : ||| :  
Db 30 LPWNSATVLOQTYHAH 45

RESULT 8  
US-08-797-689-12  
; Sequence 12, Application US/08797689  
; Patent No. 5876969  
; GENERAL INFORMATION:  
; APPLICANT: Fleer, Reinhard  
; APPLICANT: Fournier, Alain  
; APPLICANT: Guittion, Jean-Dominique  
; APPLICANT: Jung, Gerard  
; APPLICANT: Yeh, Patrice  
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,  
; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION  
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRES:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.1 (Patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/797,689  
; FILING DATE: 31-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/256,927  
; FILING DATE: 28-JUL-1994  
; APPLICATION NUMBER: FR 92/01064  
; FILING DATE: 31-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR93/00085  
; FILING DATE: 28-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith Ph.D., Julie K.  
; REGISTRATION NUMBER: P-38,619  
; REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3839  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 138 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-797-689-12

Query Match 41.3%; Score 43; DB 2; Length 138;  
Best Local Similarity 43.8%; Pred. No. 18;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MPWLSATVRSVTHAN 17  
: || ||| : : ||| :  
Db 75 LPWNSATVLOQTYHAH 90

RESULT 9  
US-09-101-272G-80  
; Sequence 80, Application US/09101272G  
; Patent No. 6509445  
; GENERAL INFORMATION:  
; APPLICANT: Nissin Food Products Co., Ltd.  
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR  
; FILE REFERENCE: Q50979  
; CURRENT APPLICATION NUMBER: US/09/101.272G  
; CURRENT FILING DATE: 1998-07-08  
; PRIOR APPLICATION NUMBER: JP 1059/1996  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 80  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ATFHI chimeric protein  
US-09-101-272G-80

Query Match 41.3%; Score 43; DB 4; Length 194;  
Best Local Similarity 43.8%; Pred. No. 26;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 MPWLSATVRSVTHAN 17  
: || ||| : : ||| :  
Db 73 LPWNSATVLOQTYHAH 88

RESULT 10  
US-09-101-272G-73  
; Sequence 73, Application US/09101272G  
; Patent No. 6509445  
; GENERAL INFORMATION:  
; APPLICANT: Nissin Food Products Co., Ltd.  
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR  
; FILE REFERENCE: Q50979  
; CURRENT APPLICATION NUMBER: US/09/101.272G  
; CURRENT FILING DATE: 1998-07-08  
; PRIOR APPLICATION NUMBER: JP 1059/1996  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 73  
; LENGTH: 200  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: ATF domain of uPA  
US-09-101-272G-73

Query Match 41.3%; Score 43; DB 4; Length 200;  
Best Local Similarity 43.8%; Pred. No. 27;  
Matches 7; Conservative 0; Gaps 0; Indels 5; Mismatches 4;

QY 2 MPWLSATTVRSVTHAN 17  
Db 92 LPWNSATVLOQTYHAH 107

## RESULT 11

US-09-101-272G-96  
; Sequence 96, Application US/09101272G  
; Patent No. 6509445  
; GENERAL INFORMATION:  
; APPLICANT: Nissin Food Products Co., Ltd.  
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR  
; FILE REFERENCE: Q50979  
; CURRENT APPLICATION NUMBER: US/09/101,272G  
; CURRENT FILING DATE: 1998-07-08  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 96  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ATFHI-CL chimeric protein  
US-09-101-272G-96

Query Match 41.3%; Score 43; DB 4; Length 201;  
Best Local Similarity 43.8%; Pred. No. 27;  
Matches 7; Conservative 0; Gaps 0; Indels 5; Mismatches 4;

QY 2 MPWLSATTVRSVTHAN 17  
Db 73 LPWNSATVLOQTYHAH 88

## RESULT 12

US-09-101-272G-98  
; Sequence 98, Application US/09101272G  
; Patent No. 6509445  
; GENERAL INFORMATION:  
; APPLICANT: Nissin Food Products Co., Ltd.  
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR  
; FILE REFERENCE: Q50979  
; CURRENT APPLICATION NUMBER: US/09/101,272G  
; CURRENT FILING DATE: 1998-07-08  
; PRIOR FILING DATE: 1996-01-08  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 98  
; LENGTH: 208  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ATFHI-ML chimeric protein  
US-09-101-272G-98

Query Match 41.3%; Score 43; DB 4; Length 208;  
Best Local Similarity 43.8%; Pred. No. 29;  
Matches 7; Conservative 0; Gaps 0; Indels 5; Mismatches 4;

QY 2 MPWLSATTVRSVTHAN 17  
Db 73 LPWNSATVLOQTYHAH 88

## RESULT 13

US-08-597-236-11  
; Sequence 11, Application US/08597236  
; Patent No. 5733765  
; GENERAL INFORMATION:  
; APPLICANT: STINGELE, Francesca  
; APPLICANT: MOLLET, Beat  
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING  
; TITLE OF INVENTION: EXOPOLYSACCHARIDES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americans  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/597,236  
; FILING DATE:  
; CLASSIFICATION: 426  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95201669.9  
; FILING DATE: 20-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fanucci A., Allan  
; REGISTRATION NUMBER: 30256  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-597-236-11

Query Match 41.3%; Score 43; DB 1; Length 360;  
Best Local Similarity 38.9%; Pred. No. 54;  
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 MPWLSATTVRSVTHANAL 19  
Db 160 MPWFILTVLATLFHATAI 177

## RESULT 14

US-08-746-682A-11  
; Sequence 11, Application US/08746682A  
; Patent No. 5786184  
; GENERAL INFORMATION:  
; APPLICANT: STINGELE, Francesca  
; APPLICANT: MOLLET, Beat  
; TITLE OF INVENTION: LACTIC BACTERIA PRODUCING  
; TITLE OF INVENTION: EXOPOLYSACCHARIDES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americans  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/746,682A  
; FILING DATE: 14-NOV-1996

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/597,236  
FILING DATE: 20-JUN-1995  
APPLICATION NUMBER: EP 95201669.9  
FILING DATE: 20-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fanucci A., Allan  
REGISTRATION NUMBER: 30256  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-746-682A-11

Query Match 41.3%; Score 43; DB 1; Length 360;

Best Local Similarity 38.9%; Pred. No. 54;  
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 2 MPWLSATTVRSVTHANAL 19  
Db 160 MPWILTVLTLFHATAI 177

RESULT 15

US-08-093-741-83  
Sequence 83, Application US/08093741  
Patent No. 5681721

GENERAL INFORMATION:

APPLICANT: STEFFENS, Gerd J.  
APPLICANT: WENDT, STEPHAN  
APPLICANT: SCHNEIDER, JOHANNES  
APPLICANT: HEINZEL-WIELAND, REGINA  
APPLICANT: SAUNDERS, DEREK J.

TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH  
TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN  
TITLE OF INVENTION: INHIBITING EFFECT

NUMBER OF SEQUENCES: 83

CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
STREET: 1200 G Street, N. W. Suite 700  
CITY: Washington, D.C.  
COUNTRY: U.S.  
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/093,741  
FILING DATE: 20-JUL-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P43 23 754.1

FILING DATE: 15-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: EVANS, Joseph D.  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 148/41345

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)628-8800

TELEFAX: (202)628-8844

INFORMATION FOR SEQ ID NO: 83:

SEQUENCE CHARACTERISTICS:

LENGTH: 365 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-093-741-83

Query Match

41.3%; Score 43; DB 1; Length 365;

Best Local Similarity 43.8%; Pred. No. 54;  
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 2 MPWLSATTVRSVTHAN 17

Db 26 LPWNSATVLOQTYHAH 41

Search completed: September 3, 2003, 11:52:26  
Job time : 16.75 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:24:37 ; Search time 48.5 Seconds  
(without alignments)  
65.454 Million cell updates/sec

Title: US-10-087-464-1

Perfect score: 104

Sequence: 1 GMPWLSATTVRSVTHANALT 20

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	104	100.0	20	23	AAE29339		Human Band 3 pepti
2	104	100.0	42	23	AAE29349		Human Band 3 prote
3	104	100.0	86	22	ABG54066		Human liver peptid
4	104	100.0	86	22	ABB39139		Peptide #6645 enco
5	104	100.0	86	22	ABB24030		Protein #6029 enco
6	104	100.0	86	22	AAW59792		Human brain expres
7	104	100.0	86	22	AAW72377		Human bone marrow
8	104	100.0	86	22	AAW32633		Peptide #6670 enco
9	104	100.0	86	23	ABG42195		Human peptide enco

10	104	100.0	911	12	AAW15355	Human erythrocyte
11	104	100.0	911	20	AAW90263	A. tigrinum AE1 pr
12	104	100.0	911	22	ABW46914	Human erythrocyte
13	104	100.0	911	23	AAE29343	Human Band 3 prote
14	104	100.0	911	23	AAE29344	Human Band 3 prote
15	104	100.0	962	22	AAU30825	Novel human secret
16	93	89.4	292	7	AAW60845	Mouse kidney cell
17	93	89.4	1240	20	AAW90262	A. tigrinum AE2 pr
18	89	85.6	1030	20	AAW90261	A. tigrinum AE3 pr
19	72	69.2	1239	22	ABB63733	Drosophila melanog
20	66	63.5	714	20	AAW74410	hNEC3 protein sequ
21	66	63.5	1032	20	AAW74409	hNEC3 protein sequ
22	66	63.5	1044	20	AAW74408	hNEC3 protein sequ
23	66	63.5	1044	21	AAW20659	Human brain-derive
24	66	63.5	1088	23	AAW47931	Murine Na+-driven
25	66	63.5	1088	23	AAW47932	Human Na+-driven C
26	66	63.5	1106	23	ABG32015	Human transporter
27	66	63.5	1129	23	ABG32014	Human transporter
28	66	63.5	1130	22	ABG03611	Novel human diagno
29	62	59.6	91	21	AAW28321	Human secreted pro
30	62	59.6	93	21	AAW28341	Human secreted pro
31	62	59.6	94	21	AAW28342	Human secreted pro
32	62	59.6	971	21	AAW11833	Human heart muscle
33	62	59.6	1000	20	AAW90274	Human NT2-2A prote
34	61	58.7	773	21	AAW23336	Drosophila Na+ dri
35	61	58.7	774	21	AAW23340	Drosophila Na+ dri
36	61	58.7	779	21	AAW23341	Drosophila Na+ dri
37	61	58.7	779	21	AAW23342	Drosophila Na+ dri
38	61	58.7	1017	22	ABB60785	Drosophila melanog
39	61	58.7	1030	21	AAW23337	Drosophila Na+ dri
40	61	58.7	1030	21	AAW23339	Drosophila Na+ dri
41	61	58.7	1086	22	ABB60786	Drosophila melanog
42	61	58.7	1086	23	ABG70008	Larval viability a
43	53	51.0	121	22	AAW25432	Human protein sequ
44	53	51.0	1074	23	ABP69139	Human polypeptide
45	53	51.0	1108	23	AAE22918	Human transporter

#### ALIGNMENTS

##### RESULT 1

AAE29339  
ID AAE29339 standard; peptide; 20 AA.

XX AC AAE29339;

XX DT 27-JAN-2003 (first entry)

XX DE Human Band 3 peptide, B35A.

XX DE Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;

XX KW Protozoacide; gene therapy.

XX OS Homo sapiens.

XX PN WO200270542-A2.

XX PD 12-SEP-2002.

XX PF 01-MAR-2002; 2002WO-US06415.

XX PR 02-MAR-2001; 2001US-272930P.

XX PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX PI Chishty AH, Oh SS, Liu B, God V;

XX DR WPI; 2002-759814/82.

XX PT New isolated Band 3 polypeptide which selectively binds to merozoite  
PT surface protein-1, useful for the prevention and treatment of malarial  
PT infection -

XX PS Claim 1; Page 84; 163pp; English.

XX CC The invention relates to an isolated Band 3 polypeptide that comprises

XX CC any of 4 20 residue amino acid sequences, or their fragments that bind

XX CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base

XX CC pair sequences. The methods and compositions of the present invention

XX CC are useful for the prevention and treatment of malarial infection. The

XX CC present invention, develops new and more improved methods based upon

XX CC inhibiting the particular interactions between the malarial parasite and

XX CC a cognate molecule present in the host and subsequently minimising

XX CC harmful side effects and drug resistance that may be due to non-specific

XX CC therapeutic approaches. The invention is useful in gene therapy. The

XX CC present invention also provides a vaccine for malaria. The present

XX CC sequence is human Band 3 peptide.

XX SQ Sequence 20 AA;

XX CC Query Match 100.0%; Score 104; DB 23; Length 20;

XX CC Best Local Similarity 100.0%; Pred. No. 2.1e-10;

XX CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 GMPWLSATTVRSVTHANALT 20

XX DB 1 GMPWLSATTVRSVTHANALT 20

XX CC RESULT 2

XX CC AAE29349

XX ID AAE29349 standard; peptide; 42 AA.

XX CC AAE29349;

XX DT 27-JAN-2003 (first entry)

XX DE Human Band 3 protein ectoplasmic domain 5.

XX KW Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;

XX KW protozoacide; gene therapy.

XX OS Homo sapiens.

XX PN WO200270542-A2.

XX PD 12-SEP-2002.

XX PF 01-MAR-2002; 2002WO-US06415.

XX PR 02-MAR-2001; 2001US-272930P.

XX FA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX PI Chishti AH, Oh SS, Liu D, Goel V;

XX DR WPI; 2002-759814/82.

XX FT New isolated Band 3 polypeptide which selectively binds to merozoite

XX FT surface protein-1, useful for the prevention and treatment of malarial

XX FT infection -

XX PS Example; Page 58; 163pp; English.

XX CC The invention relates to an isolated Band 3 polypeptide that comprises

XX CC any of 4 20 residue amino acid sequences, or their fragments that bind

XX CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base

XX CC pair sequences. The methods and compositions of the present invention

XX CC are useful for the prevention and treatment of malarial infection. The

XX CC present invention, develops new and more improved methods based upon

XX CC inhibiting the particular interactions between the malarial parasite and

XX CC a cognate molecule present in the host and subsequently minimising

XX CC harmful side effects and drug resistance that may be due to non-specific

XX CC therapeutic approaches. The invention is useful in gene therapy. The

XX CC present invention also provides a vaccine for malaria. The present

XX CC sequence is human Band 3 protein ectoplasmic domain 5.

XX SQ Sequence 42 AA;

XX CC Query Match 100.0%; Score 104; DB 23; Length 42;

XX CC Best Local Similarity 100.0%; Pred. No. 5.1e-10;

XX CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 GMPWLSATTVRSVTHANALT 20

XX DB 1 GMPWLSATTVRSVTHANALT 20

XX CC RESULT 3

XX CC ABG54066

XX ID ABG54066 standard; Peptide; 86 AA.

XX AC ABG54066;

XX DT 25-FEB-2003 (first entry)

XX DE Human liver peptide, SEQ ID No 32714.

XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;

XX KW hypercholesterolaemia; coronary heart disease.

XX OS Homo sapiens.

XX PN WO200157273-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US00664.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX FA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488898/53.

XX FT Human genome-derived single exon nucleic acid probes useful for

XX FT analysing gene expression in human adult liver -

XX PS Claim 27; SEQ ID No 32714; 658pp; English.

XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for

XX CC measuring human gene expression in a sample derived from human adult

XX CC liver, comprising one of 13109 defined nucleotide sequences given in the

XX CC specification (or complements/ fragments). The probe hybridises at high

XX CC stringency to a nucleic acid molecule expressed in the human adult

XX CC liver. (I) may be used for predicting, measuring and displaying gene

XX CC expression in samples derived from human adult liver. The genes

XX CC identified may be involved in genetic liver diseases such as cirrhosis,

XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which

XX CC is associated with coronary heart disease. ABG47348-ABG59930 represent

XX CC human liver single exon encoded peptides of the invention.

XX CC Note: The sequence information for this patent does not appear in the

XX CC printed specification but was obtained in electronic format directly

XX CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 86 AA;

XX CC Query Match 100.0%; Score 104; DB 22; Length 86;

XX CC Best Local Similarity 100.0%; Pred. No. 1.2e-09;

XX CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

XX XX Protein #6029 encoded by probe for measuring heart cell gene expression.
XX DE
XX DE Human; gene expression; heart; microarray; vascular system;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200157274-A2.
XX XX
XX PD 09-AUG-2001.
XX XX
XX XX 30-JAN-2001; 2001WO-US000666.
XX XX
XX XX 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX XX
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI
XX XX WPI; 2001-488899/53.
XX DR
XX XX
XX XX Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts -
XX XX
XX XX Claim 15; SEQ ID NO 25800; 530pp; English.
XX XX
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart (see
XX CC ABA21335-ABA41305). The present sequence is a protein encoded by one such
XX CC probe. The probes may be used for predicting, measuring and displaying
XX CC gene expression in samples derived from the human heart via microarrays.
XX CC By measuring gene expression, the probes are useful for predicting,
XX CC diagnosing, grading, staging, monitoring and prognosing diseases of the
XX CC human heart and vascular system e.g. cardiovascular disease,
XX CC hypertension, cardiac arrhythmias and congenital heart disease.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX XX Sequence 86 AA;
XX XX
XX XX
XX XX Query Match 100.0%; Score 104; DB 22; Length 86;
XX XX Best Local Similarity 100.0%; Pred. No. 1.2e-09;
XX XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1 GMPWLSATTVRSVTHANALT 20
XX XX
XX DB 34 GMPWLSATTVRSVTHANALT 53
XX XX
XX XX
XX XX RESULT 6
XX XX AAM59792
XX XX ID AAM59792 standard; Protein; 86 AA.
XX XX
XX XX AAM59792;
XX XX
XX XX
XX XX 05-NOV-2001 (first entry)
XX XX
XX XX Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.
XX DE
XX DE Human; brain expressed exon; gene expression analysis; probe;
XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer.
XX XX
XX OS Homo sapiens.

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XX PN W0200157275-A2.
XX XX
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US00667.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483446/52.
XX XX
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains -
XX PS Example 4; SEQ ID NO: 31897; 650pp + Sequence Listing; English.
XX CC
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention.
XX SQ Sequence 86 AA;
XX
XX Query Match 100.0%; Score 104; DB 22; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-09;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GMPWLSATTVRSVTHANALT 20
XX Db ||||| ||||| ||||| ||||| |||||
XX 34 GMPWLSATTVRSVTHANALT 53
XX
XX RESULT 7
XX AAM72377
XX ID AAM72377 standard; Protein; 86 AA.
XX AC AAM72377;
XX XX
XX DT 06-NOV-2001 (first entry)
XX XX
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32683.
XX XX
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX XX
XX OS Homo sapiens.
XX XX
XX PN W0200157276-A2.
XX XX
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US00668.
XX XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488897/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human placenta -
XX PS Claim 27; SEQ ID NO 32902; 654pp; English.
XX XX
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AA131315-AA157546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for

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XX XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488900/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human bone marrow -
XX PS Example 4; SEQ ID NO: 32683; 658pp + Sequence Listing; English.
XX XX
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention.
XX SQ Sequence 86 AA;
XX
XX Query Match 100.0%; Score 104; DB 22; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-09;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GMPWLSATTVRSVTHANALT 20
XX Db ||||| ||||| ||||| ||||| |||||
XX 34 GMPWLSATTVRSVTHANALT 53
XX
XX RESULT 8
XX AAM32633
XX ID AAM32633 standard; Protein; 86 AA.
XX AC AAM32633;
XX XX
XX DT 17-OCT-2001 (first entry)
XX XX
XX DE Peptide #670 encoded by probe for measuring placental gene expression.
XX XX
XX KW Probe; microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX XX
XX OS Homo sapiens.
XX XX
XX PN W0200157272-A2.
XX XX
XX PD 09-AUG-2001.
XX XX
XX PF 30-JAN-2001; 2001WO-US00663.
XX XX
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX XX
XX DR WPI; 2001-488897/53.
XX XX
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human placenta -
XX PS Claim 27; SEQ ID NO 32902; 654pp; English.
XX XX
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AA131315-AA157546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for

```

CC predicting, measuring and displaying gene expression in samples derived  
 CC from human placenta. The probes are useful for antenatal diagnosis of  
 CC human genetic disorders.

XX Sequence 86 AA;

XX Query Match 100.0%; Score 104; DB 22; Length 86;  
 XX Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
 Db 34 GMPWLSATTVRSVTHANALT 53

RESULT 9

ID ABG42195 standard; Peptide: 86 AA.

AC ABG42195;

DT 19-AUG-2002 (first entry)

DE Human peptide encoded by genome-derived single exon probe SEQ ID 31860.

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.

OS Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US000665.

XX 04-FEB-2000; 2000US-180312P.

XX 26-MAY-2000; 2000US-207456P.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-234687P.

XX 27-SEP-2000; 2000US-236359P.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to

XX measure gene expression in human lung samples -

XX Claim 27; SEQ ID No 31860; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon

XX nucleic acid probes for measuring gene expression in a sample derived

XX from human lung comprising single exon nucleic acid probes having one of

XX 12614 nucleic acid sequences mentioned in the specification, or their

XX complements or the 12387 open reading frames derived from the 12614

XX probes. Also included are a microarray comprising the novel set of

XX probes; the novel set of probes which hybridise at high stringency to a

XX nucleic acid expressed in the human lung; measuring gene expression in a

XX sample derived from human lung, comprising (a) contacting the array with

XX a collection of detectably labeled nucleic acids derived from human lung

XX mRNA, and (b) measuring the label detectably bound to each probe of

CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene  
 CC expression analysis, and for identifying exons in a gene, particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a peptide/protein  
 CC encoded by a single exon probe of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 86 AA;

XX Query Match 100.0%; Score 104; DB 23; Length 86;  
 XX Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
 Db 34 GMPWLSATTVRSVTHANALT 53

RESULT 10

AARI5355

ID AARI5355 standard; Protein: 911 AA.

AC AARI5355;

XX 25-MAR-2003 (updated)

DT 08-MAR-1992 (first entry)

XX Human erythrocyte membrane anion-transport protein (band 3).

XX Senescent cell peptide; ANION 1; COOH; auto immune disease.

XX Homo sapiens.

XX WO9118013-A.

XX 28-NOV-1991.

XX 24-MAY-1991; 91WO-US03557.

XX 24-MAY-1990; 90US-0528210.

XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.

XX Kay MBM, Marchalonis JJ;

XX WPI; 1991-369184/50.

XX N-PSDB; AAQ15172.

XX Synthetic senescent cell antigen and peptide(s) - used to detect

XX antibodies to SCA, study cellular ageing and auto-immune



CC physiological effect of a composition comprising hemoglobin which  
 CC involves obtaining electron paramagnetic resonance (EPR) or UV spectra of  
 CC iron-nitrosyl hemoglobin derivatives formed by incubation of limiting  
 CC nitric oxide (NO) with hemoglobin and determining if the composition  
 CC shows non-cooperativity or cooperativity in binding of NO to the  
 CC hemoglobin. The products of the invention have antianemic; antibacterial;  
 CC immunosuppressive; vasotropic; antiinflammatory; antithrombotic;  
 CC respiratory; antithrombotic and cerebroprotective activity. The products  
 CC of the invention are used to produce methods of therapy for medical  
 CC disorders characterized by red blood cell membrane defects and for a  
 CC variety of hypercoagulable and vasculopathic states, particularly for  
 CC patients with septic shock who develop myocardial depression,  
 CC pancreatitis and progressive respiratory failure, patients with  
 CC septicemia as a complication of urinary tract infection and patients with  
 CC ischemia, patients in a sickle cell crisis and for treating inflammatory  
 CC conditions such as arthritis, asthma, cerebritis, bronchitis and  
 CC vasculitis. The methods are also used for preserving red blood cells  
 CC which can be used in therapy.

XX Sequence 911 AA;  
 Query Match 100.0%; Score 104; DB 22; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT.20  
 DB 720 GMPWLSATTVRSVTHANALT 739  
 |||||

RESULT 13  
 AAE29343  
 ID AAE29343 standard; Protein; 911 AA.

XX AC AAE29343;  
 XX DT 27-JAN-2003 (first entry)  
 XX DE Human Band 3 protein #1.  
 XX KW Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
 XX KW protozoacide; gene therapy.

XX OS Homo sapiens.

XX PN WO200270542-A2.

XX PD 12-SEP-2002.

XX PF 01-MAR-2002; 2002WO-US06415.

XX PR 02-MAR-2001; 2001US-272930P.

XX PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX PI Chishtli AH, Oh SS, Liu D, Goel V;

XX DR WPI; 2002-759814/82.

XX DR N-PSDB; AAD46978.

XX PT New isolated Band 3 polypeptide which selectively binds to merozoite  
 PT surface protein-1, useful for the prevention and treatment of malarial  
 PT infection -

XX PS Disclosure; Page 102-105; 163pp; English.

XX CC The invention relates to an isolated Band 3 polypeptide that comprises  
 CC any of 4 20 residue amino acid sequences, or their fragments that bind  
 CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
 CC pair sequences. The methods and compositions of the present invention  
 CC are useful for the prevention and treatment of malarial infection. The  
 CC present invention, develops new and more improved methods based upon  
 CC inhibiting the particular interactions between the malarial parasite and

CC a cognate molecule present in the host and subsequently minimising  
 CC harmful side effects and drug resistance that may be due to non-specific  
 CC therapeutic approaches. The invention is useful in gene therapy. The  
 CC present invention also provides a vaccine for malaria. The present  
 CC sequence is human Band 3 protein.

XX Sequence 911 AA;

Query Match 100.0%; Score 104; DB 23; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
 DB 720 GMPWLSATTVRSVTHANALT 739  
 |||||

RESULT 14  
 AAE29344  
 ID AAE29344 standard; Protein; 911 AA.

XX AC AAE29344;

XX DT 27-JAN-2003 (first entry)

XX DE Human Band 3 protein #2.

XX KW Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
 XX KW protozoacide; gene therapy.

XX OS Homo sapiens.

XX PN WO200270542-A2.

XX PD 12-SEP-2002.

XX PF 01-MAR-2002; 2002WO-US06415.

XX PR 02-MAR-2001; 2001US-272930P.

XX PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX PI Chishtli AH, Oh SS, Liu D, Goel V;

XX DR WPI; 2002-759814/82.

XX DR N-PSDB; AAD46979.

XX PT New isolated Band 3 polypeptide which selectively binds to merozoite  
 PT surface protein-1, useful for the prevention and treatment of malarial  
 PT infection -

XX PS Disclosure; Page 107-110; 163pp; English.

XX CC The invention relates to an isolated Band 3 polypeptide that comprises  
 CC any of 4 20 residue amino acid sequences, or their fragments that bind  
 CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
 CC pair sequences. The methods and compositions of the present invention  
 CC are useful for the prevention and treatment of malarial infection. The  
 CC present invention, develops new and more improved methods based upon  
 CC inhibiting the particular interactions between the malarial parasite and  
 CC a cognate molecule present in the host and subsequently minimising  
 CC harmful side effects and drug resistance that may be due to non-specific  
 CC therapeutic approaches. The invention is useful in gene therapy. The  
 CC present invention also provides a vaccine for malaria. The present  
 CC sequence is human Band 3 protein.

XX Sequence 911 AA;

Query Match 100.0%; Score 104; DB 23; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20

```

Db      720 GMPWLSATTVRSVTHANALT 739
|||||
RESULT 15
AAU30825
ID      AAU30825 standard; Protein; 962 AA.
XX
AC      AAU30825;
XX
DT      18-DEC-2001 (first entry)
XX
DE      Novel human secreted protein #1316.
XX
KW      Human; vaccination; gene therapy; nutritional supplement;
KW      stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW      immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS      Homo sapiens.
XX
PN      WO200179449-A2.
XX
PD      25-OCT-2001.
XX
PF      16-APR-2001; 2001WO-US08656.
XX
PR      18-APR-2000; 2000US-0552929.
XX
PR      26-JAN-2001; 2001US-0770160.
XX
PA      (HYSE-) HYSEQ INC.
XX
PI      Tang YT, Liu C, Drmanac RT;
XX
WPI; 2001-611725/70.
XX
Nucleic acids encoding a range of human polypeptides, useful in genetic
PT. vaccination, testing and therapy -
XX
PS      Claim 20; Page 354; 765pp; English.
XX
CC      The invention relates to novel human secreted polypeptides. The
CC      polypeptides and antibodies to the polypeptides are useful for
CC      determining the presence of or predisposition to a disease associated
CC      with altered levels of polypeptide. The polypeptides are also useful for
CC      identifying agents (agonists and antagonists) that bind to them. Cells
CC      expressing the proteins are useful for identifying a therapeutic agent
CC      for use in treatment of a pathology related to aberrant expression or
CC      physiological interactions of the polypeptide. Vectors comprising
CC      the nucleic acids encoding the polypeptides and cells genetically
CC      engineered to express them are also useful for producing the proteins.
CC      The proteins are useful in genetic vaccination, testing and
CC      therapy, and can be used as nutritional supplements. They may be used to
CC      increase stem cell proliferation; to regulate haematopoiesis; and in
CC      bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC      immune suppression and/or stimulation; as anti-inflammatory agents; and
CC      in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC      sequences of novel human secreted proteins of the invention.
XX
SQ      Sequence 962 AA;
Query Match 100.0%; Score 104; DB 22; Length 962;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 GMPWLSATTVRSVTHANALT 20
|||||
Db      771 GMPWLSATTVRSVTHANALT 790

```

Search completed: September 3, 2003, 11:46:11  
 Job time : 50.5 secs



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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:40:18 ; Search time 44.5 Seconds  
(without alignments)  
115.979 Million cell updates/sec

Title: US-10-087-464-2

Perfect score: 98

Sequence: 1 SVTHANALTMGKASTPGAA 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	92.9	849	11 Q91ZE7	Q91ze7 rattus norv
2	79	80.6	855	6 Q9TUQ0	Q9tuq0 bos taurus
3	79	80.6	930	6 Q9XSW5	Q9xsw5 bos taurus
4	73	74.5	103	11 Q35225	Q35225 cynomys lud
5	73	74.5	466	11 Q99LT5	Q99lt5 mus musculu
6	73	74.5	622	6 Q9TU75	Q9tu75 sus scrofa
7	73	74.5	1159	4 Q8TAG3	Q8tag3 homo sapien
8	73	74.5	1219	13 Q90710	Q90710 gallus gall
9	73	74.5	1227	4 Q9UEY4	Q9uey4 homo sapien
10	73	74.5	1232	4 Q9UEY5	Q9uey5 homo sapien
11	73	74.5	1241	4 Q99654	Q99654 homo sapien
12	73	74.5	1241	4 Q9UEY6	Q9uey6 homo sapien
13	72	73.5	160	13 P79877	P79877 lampetra ja
14	71	72.4	844	13 Q90579	Q90579 gallus gall
15	67	68.4	124	4 Q9UDJ1	Q9udj1 homo sapien
16	63	64.3	912	13 Q91452	Q91452 oncorhynch

17	61	62.2	812	13	Q8JFT9	Q8jft9 brachydanio
18	61	62.2	1030	11	Q9ERP4	Q9erp4 mus musculu
19	61	62.2	1227	11	Q9ERP5	Q9erp5 mus musculu
20	57	58.2	357	4	Q99416	Q99416 homo sapien
21	57	58.2	357	4	Q13717	Q13717 homo sapien
22	51	52.0	467	5	Q95SW2	Q95sw2 drosophila
23	51	52.0	914	5	Q8MRK3	Q8mrk3 drosophila
24	51	52.0	1161	5	Q8IQD4	Q8iqd4 drosophila
25	51	52.0	1201	5	Q8IQD6	Q8iqd6 drosophila
26	51	52.0	1228	5	Q8IQD5	Q8iqd5 drosophila
27	51	52.0	1268	5	Q9VT48	Q9vt48 drosophila
28	49	50.0	450	10	Q8GZWL	Q8gzwl oryza sativ
29	47.5	48.5	409	16	Q92VY7	Q92vy7 rhizobium m
30	47	48.0	1044	4	Q95233	Q95233 homo sapien
31	47	48.0	1087	11	Q8CFS3	Q8cfs3 mus musculu
32	47	48.0	1088	4	Q9HCQ6	Q9hqc6 homo sapien
33	47	48.0	1088	11	Q9EST0	Q9est0 mus musculu
34	47	48.0	1088	11	Q8C943	Q8c943 mus musculu
35	47	48.0	1089	11	Q9JKV6	Q9jkv6 mus musculu
36	47	48.0	1089	11	Q8JZR6	Q8jzr6 mus musculu
37	47	48.0	1089	11	Q8BYI7	Q8byi7 mus musculu
38	47	48.0	1130	4	Q94843	Q94843 homo sapien
39	47	48.0	1613	2	Q9KKB2	Q9kkb2 israeli tic
40	47	48.0	1614	2	Q9KKB6	Q9kkb6 astrakhan r
41	47	48.0	1615	2	Q9KKA4	Q9kka4 rickettsia
42	47	48.0	1616	2	Q9KKA9	Q9kka9 rickettsia
43	47	48.0	1616	2	Q9KKA7	Q9kka7 rickettsia
44	47	48.0	1616	2	Q9KKB8	Q9kkb8 rickettsia
45	46	46.9	651	11	Q8BWZ4	Q8bwz4 mus musculu

## ALIGNMENTS

RESULT 1

Q91ZE7 ID Q91ZE7 PRELIMINARY; PRT; 849 AA.

AC Q91ZE7;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Band 3 anion exchange protein.

OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Ye-H., Binder H.J., Rajendran V.M.;  
RT "Molecular cloning and characterization of band 3 anion exchange protein (AE1) mRNA from rat colon."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY030082; RAK38733.1; -;  
DR InterPro; IPR001717; Anion\_exchange.  
DR InterPro; IPR003020; HCO3\_cotransp.  
DR Pfam; PF00955; HCO3\_cotransp; 1.  
DR PRINTS; PR01231; HCO3TRNSPORT.  
DR TIGRFAms; TIGR00834; ae; 1.  
DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
SQ SEQUENCE 849 AA; 94312 MW; E4B200780CB07D3A CRC64;

Query Match 92.9%; Score 91; DB 11; Length 849;

Best Local Similarity 95.0%; Pred.No. 3.7e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVTHANALTMGKASTPGAA 20

Db 669 SVTHANALTMGKASPGAA 688

RESULT 2

```
Q9TU00
ID Q9TU00 PRELIMINARY; PRT; 855 AA.
AC Q9TU00;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Band 3 protein.
GN BKB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Koshino I., Inaba M., Matsumoto M., Ono K.;
RT "Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated
RT with decreased mutant mRNA possessing dominant negative effect and
RT dominant hereditary spherocytosis in cattle.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF163828; AAD43354.1; -.
DR HSSP; P02730; 1BNX.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 855 AA; 95643 MW; 06CD037324F69872 CRC64;

Query Match 80.6%; Score 79; DB 6; Length 855;
Best Local Similarity 84.2%; Pred. No. 0.00034;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPCA 19
Db 674 TVTHANALTMVKDSTPCA 692

RESULT 3
Q9XSW5
ID Q9XSW5 PRELIMINARY; PRT; 930 AA.
AC Q9XSW5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Band 3 protein.
GN BEB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Koshino I., Inaba M., Matsumoto M., Ono K.;
RT "Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated
RT with decreased mutant mRNA possessing dominant negative effect and
RT dominant hereditary spherocytosis in cattle.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF163826; AAD43593.1; -.
DR HSSP; P02730; 1BNX.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 930 AA; 104374 MW; 4F6AADFEB6AF6A3A1 CRC64;
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Query Match 80.6%; Score 79; DB 6; Length 930;
Best Local Similarity 84.2%; Pred. No. 0.00037;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPCA 19
Db 749 TVTHANALTMVKDSTPCA 767

RESULT 4
Q35225
ID Q35225 PRELIMINARY; PRT; 103 AA.
AC Q35225;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anion exchange protein 2 (Fragment).
GN AE-2.
OS Cynomys ludovicianus (Black-tailed prairie dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Cynomys.
OC NCBI_TaxID=45480;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gall bladder;
RA Abedin Z.R., Moser A.J., Roslyn J.J., Abedin M.Z.;
RT "Expression of anion exchange protein 2 (AE-2) in gallbladder
RT epithelia.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF012895; AAB66833.1; -.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR NON_TER 1
DR NON_TER 103
SQ SEQUENCE 103 AA; 11012 MW; 29A99247E768B455 CRC64;

Query Match 74.5%; Score 73; DB 11; Length 103;
Best Local Similarity 83.3%; Pred. No. 0.00035;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPCA 18
Db 55 SVTHANALTMVKAVAPG 72

RESULT 5
Q99LT5
ID Q99LT5 PRELIMINARY; PRT; 466 AA.
AC Q99LT5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein (Fragment).
GN SLC4A2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002234; AAH02234.1; -.
DR MGD; MGI:109351; SLC4a2.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Hypothetical protein.
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FT NON_TER 1 1
SQ SEQUENCE 466 AA; 52003 MW; 481C1108E28D03B1 CRC64;

Query Match
Best Local Similarity 74.5%; Score 73; DB 11; Length 466;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPG 18
DB 286 SVTHANALTMVKAVPG 303

RESULT 6
Q9TU75 PRELIMINARY; PRT; 622 AA.
AC Q9TU75;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Chloride-bicarbonate anion exchanger AE2 (Fragment).
GN AE2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=96339307; PubMed=8756692;
RA Zolotarev A.S., Chernova M.N., Yannoukakos D., Alper S.L.;
RT "Proteolytic cleavage sites of native AE2 anion exchanger in gastric
mucosal membranes.";
RL Biochemistry 35:10367-10376(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=99315230; PubMed=10387099;
RA Zolotarev A.S., Shmukler B.E., Alper S.L.;
RT "AE2 anion exchanger polypeptide is a homooligomer in pig gastric
membranes: a chemical cross-linking study.";
RL Biochemistry 38:8521-8531(1999).
DR EMBL; AF120099; AAF00977.1; -.
DR HSSP; P02730; lBTQ.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
FT NON_TER 1 1
SQ SEQUENCE 622 AA; 68713 MW; 58B013462C36E1DC CRC64;

Query Match
Best Local Similarity 74.5%; Score 73; DB 6; Length 622;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPG 18
DB 442 SVTHANALTMVKAVPG 459

RESULT 7
Q8TAG3 PRELIMINARY; PRT; 1159 AA.
AC Q8TAG3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to solute carrier family 4, anion exchanger, member 2
(Erythrocyte membrane protein band 3-like 1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028601; AAB28601.1; -.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 1159 AA; 127747 MW; 9F083A2BE8FF5D74 CRC64;

Query Match
Best Local Similarity 74.5%; Score 73; DB 4; Length 1159;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPG 18
DB 979 SVTHANALTMVKAVPG 996

RESULT 8
Q90710 PRELIMINARY; PRT; 1219 AA.
AC Q90710;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE AE2-1 anion exchanger.
GN AE2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Proventriculus;
RX MEDLINE=96224107; PubMed=8621532;
RA Cox K.H., Adair-Kirk T.L., Cox J.V.;
RT "Variant AE2 anion exchanger transcripts accumulate in multiple cell
types in the chicken gastric epithelium.";
RL J. Biol. Chem. 271:8995-8902(1996).
DR EMBL; U48889; AAC59881.1; -.
DR HSSP; P02730; lBTQ.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 1219 AA; 135288 MW; 25F42A73C3483B21 CRC64;

Query Match
Best Local Similarity 74.5%; Score 73; DB 13; Length 1219;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPG 18
DB 1040 SVTHANALTMVKAVPG 1057

RESULT 9
Q9UEY4 PRELIMINARY; PRT; 1227 AA.
AC Q9UEY4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

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DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Anion exchanger 2 type b1.  
 GN SLC4A2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97179202; PubMed=9027488;  
 RA Medina J.F., Lecanda J., Acin A., Ciesielezyk P., Prieto J.;  
 RT "Tissue-specific N-terminal isoforms from overlapping alternate  
 promoters of the human AE2 anion exchanger gene.";  
 RL Biochem. Biophys. Res. Commun. 267:228-235(2000).  
 DR EMBL; U76669; AAF19584.2;  
 DR EMBL; U76667; AAF19584.2; JOINED.  
 DR EMBL; U76668; AAF19584.2; JOINED.  
 DR HSSP; P02730; IBTQ.  
 DR InterPro; IPR001717; Anion\_exchanger.  
 DR PFam; PF00955; HCO3\_cotransp.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1227 AA; 135577 MW; 5D47714C17FB8EF7 CRC64;  
  
 Query Match 74.5%; Score 73; DB 4; Length 1227;  
 Best Local Similarity 83.3%; Pred. No. 0.0047;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 1 SVTHANALTMVGKASTPG 18  
 Db 1047 SVTHANALTMVSKAVAPG 1064  
  
 RESULT 10  
 Q9UEY5 ID Q9UEY5 PRELIMINARY; PRT; 1232 AA.  
 AC Q9UEY5;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Anion exchanger 2 type b2.  
 GN SLC4A2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97179202; PubMed=9027488;  
 RA Medina J.F., Acin A., Prieto J.;  
 RT "Molecular cloning and characterization of the human AE2 anion  
 exchanger (SLC4A2) gene.";  
 RL Genomics 39:74-85(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20090621;  
 RA Medina J.F., Lecanda J., Acin A., Ciesielezyk P., Prieto J.;  
 RT "Tissue-specific N-terminal isoforms from overlapping alternate  
 promoters of the human AE2 anion exchanger gene.";  
 RL Biochem. Biophys. Res. Commun. 267:228-235(2000).  
 DR EMBL; U76669; AAF23240.1;  
 DR EMBL; U76667; AAF23240.1; JOINED.  
 DR EMBL; U76668; AAF23240.1; JOINED.

DR HSSP; P02730; IBTQ.  
 DR InterPro; IPR001717; Anion\_exchanger.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR PFam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1232 AA; 136218 MW; 22688C662907C2D7 CRC64;  
  
 Query Match 74.5%; Score 73; DB 4; Length 1232;  
 Best Local Similarity 83.3%; Pred. No. 0.0047;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 1 SVTHANALTMVGKASTPG 18  
 Db 1052 SVTHANALTMVSKAVAPG 1069  
  
 RESULT 11  
 Q99654 ID Q99654 PRELIMINARY; PRT; 1241 AA.  
 AC Q99654;  
 DT 01-MAY-1997 (TReMBLrel. 03, Created)  
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE AE2 anion exchanger.  
 GN SLC4A2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97179202; PubMed=9027488;  
 RA Medina J.F., Acin A., Prieto J.;  
 RT "Molecular cloning and characterization of the human AE2 anion  
 exchanger (SLC4A2) gene.";  
 RL Genomics 39:74-85(1997).  
 DR EMBL; U62531; AAC50964.1; -.  
 DR HSSP; P02730; IBTQ.  
 DR InterPro; IPR001717; Anion\_exchanger.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR PFam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1241 AA; 137009 MW; D266ECDAB238FD97 CRC64;  
  
 Query Match 74.5%; Score 73; DB 4; Length 1241;  
 Best Local Similarity 83.3%; Pred. No. 0.0047;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 1 SVTHANALTMVGKASTPG 18  
 Db 1061 SVTHANALTMVSKAVAPG 1078  
  
 RESULT 12  
 Q9UEY6 ID Q9UEY6 PRELIMINARY; PRT; 1241 AA.  
 AC Q9UEY6;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE Anion exchanger 2 type a.  
 GN SLC4A2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97179202; PubMed=9027488;  
 RA Medina J.F., Acin A., Prieto J.;  
 RT "Molecular cloning and characterization of the human AE2 anion  
 RL exchanger (SLC4A2) gene.";  
 RN Genomics 39:74-85(1997).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20090621;  
 RA Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;  
 RT "Tissue-specific N-terminal isoforms from overlapping alternate  
 RL promoters of the human AE2 anion exchanger gene.";  
 DR EMBL; U76669; AAF19583.2; -;  
 DR EMBL; U76667; AAF19583.2; JOINED.  
 DR EMBL; U76668; AAF19583.2; JOINED.  
 DR HSSP; P02730; 1BQ.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1241 AA; 136980 MW; D2FDA72E20D70D64 CRC64;

Query Match 74.5%; Score 73; DB 4; Length 1241;  
 Best Local Similarity 83.3%; Pred. No. 0.0047;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPG 18  
 ||||| ||||| || ||  
 DB 1061 SVTHANALTMVSKAVPG 1078

## RESULT 13

P79877  
 ID P79877 PRELIMINARY; PRT; 160 AA.  
 AC P79877;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-WAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Major anion transport protein band 3 (Fragment).  
 OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Lethenteron.  
 OX NCBI\_TaxID=94989;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96089372; PubMed=8535177;  
 RA Kay M.M., Cover C., Schluter S.F., Bernstein R.M., Marchalonis J.J.;  
 RT "Band 3, the anion transporter, is conserved during evolution:  
 RT implications for aging and vertebrate evolution.";  
 RL Cell. Mol. Biol. 41:833-842(1995).  
 DR EMBL; S80168; AADI4330.1; -;  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 160 AA; 17329 MW; A5EE8C029518A2B8 CRC64;

Query Match 73.5%; Score 72; DB 13; Length 160;  
 Best Local Similarity 77.8%; Pred. No. 0.00081;  
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPG 18  
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 DB 107 SVTHVNALTMVSKATAPG 124

## RESULT 14

Q90579  
 ID Q90579 PRELIMINARY; PRT; 844 AA.  
 AC Q90579;

DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Erythroid anion transporter.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88216609; PubMed=2835670;  
 RA Cox J.V., Lazariades E.;  
 RT "Alternative primary structures in the transmembrane domain of the  
 RL chicken erythroid anion transporter.";  
 DR EMBL; M19496; AAA48604.1; -;  
 DR HSSP; P02730; 1BQ.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 844 AA; 93808 MW; C463F993D5974276 CRC64;

Query Match 72.4%; Score 71; DB 13; Length 844;  
 Best Local Similarity 66.7%; Pred. No. 0.0067;  
 Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPG 18  
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 DB 664 TITHANALTMVCKSAVPG 681

## RESULT 15

Q9UDJ1  
 ID Q9UDJ1 PRELIMINARY; PRT; 124 AA.  
 AC Q9UDJ1;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Band 3 protein (Fragments).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92406862; PubMed=1527044;  
 RA Kang D., Okubo K., Hamasaki N., Kuroda N., Shiraki H.;  
 RT "A structural study of the membrane domain of band 3 by tryptic  
 RT digestion. Conformational change of band 3 in situ induced by alkali  
 RT treatment.";  
 RL J. Biol. Chem. 267:19211-19217(1992).  
 FT NON\_TER 1  
 FT NON\_CONS 12  
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 SQ SEQUENCE 124 AA; 13001 MW; E2028D64A8E4A4D1 CRC64;

Query Match 68.4%; Score 67; DB 4; Length 124;  
 Best Local Similarity 93.3%; Pred. No. 0.0041;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKAS 15

Search completed: September 3, 2003, 11:50:03  
Job time : 46.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:46:23 ; Search time 17.5 Seconds  
(without alignments)  
156.918 Million cell updates/sec

Title: US-10-087-464-2

Perfect score: 98

Sequence: 1 SVTHANALTMVKASTPGAA 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	98	100.0	20	15 US-10-087-464-2	Sequence 2, Appli
2	98	100.0	42	15 US-10-087-464-22	Sequence 22, Appl
3	98	100.0	86	9 US-09-864-761-39328	Sequence 39328, A
4	98	100.0	911	15 US-10-066-320-2	Sequence 2, Appli
5	98	100.0	911	15 US-10-087-464-6	Sequence 6, Appli
6	98	100.0	911	15 US-10-087-464-8	Sequence 8, Appli
7	49	50.0	262	9 US-09-815-242-10954	Sequence 10954, A
8	49	50.0	262	15 US-10-260-877-2	Sequence 2, Appli
9	47	48.0	714	9 US-09-728-137-4	Sequence 4, Appli
10	47	48.0	1032	9 US-09-728-137-8	Sequence 8, Appli
11	47	48.0	1044	9 US-09-728-137-2	Sequence 2, Appli
12	47	48.0	1085	9 US-09-734-674-4	Sequence 4, Appli
13	47	48.0	1085	15 US-10-274-990-4	Sequence 4, Appli
14	47	48.0	1088	9 US-09-920-804-2	Sequence 2, Appli
15	47	48.0	1088	9 US-09-920-804-4	Sequence 4, Appli

16	47	48.0	1129	9	US-09-734-674-2	Sequence 2, Appli
17	47	48.0	1129	15	US-10-274-990-2	Sequence 2, Appli
18	46	46.9	860	10	US-09-738-626-5357	Sequence 5357, Ap
19	45	45.9	20	15	US-10-087-464-3	Sequence 3, Appli
20	44	44.9	20	15	US-10-087-464-1	Sequence 1, Appli
21	44	44.9	272	10	US-09-925-300-1450	Sequence 1450, Ap
22	43	43.9	526	9	US-09-855-134-2	Sequence 2, Appli
23	42	42.9	4551	11	US-09-793-708-1	Sequence 1, Appli
24	42	42.9	4551	12	US-10-201-365-2	Sequence 2, Appli
25	42	42.9	4551	12	US-10-160-539-1	Sequence 1, Appli
26	42	42.9	4613	10	US-09-861-289-31	Sequence 31, Appli
27	42	42.9	4613	10	US-09-860-846-31	Sequence 31, Appli
28	42	42.9	4613	11	US-09-988-384B-31	Sequence 31, Appli
29	42	42.9	4613	11	US-09-836-821-31	Sequence 31, Appli
30	42	42.9	11877	10	US-09-861-289-6	Sequence 6, Appli
31	42	42.9	11877	10	US-09-860-846-6	Sequence 6, Appli
32	42	42.9	11877	11	US-09-836-821-6	Sequence 6, Appli
33	42	42.9	12199	11	US-09-988-384B-6	Sequence 6, Appli
34	41.5	42.3	536	9	US-09-815-242-4978	Sequence 4978, Ap
35	41.5	42.3	563	9	US-09-815-242-10841	Sequence 10841, A
36	41	41.8	185	10	US-09-738-626-6392	Sequence 6392, Ap
37	41	41.8	395	9	US-09-160-116-15	Sequence 15, Appl
38	41	41.8	399	9	US-09-160-116-12	Sequence 12, Appl
39	41	41.8	1073	10	US-09-738-626-4365	Sequence 4365, Ap
40	41	41.8	1643	10	US-09-738-626-6894	Sequence 6894, Ap
41	40	40.8	222	9	US-09-832-197-5	Sequence 5, Appli
42	40	40.8	294	15	US-10-106-698-6379	Sequence 6379, Ap
43	40	40.8	307	15	US-10-156-761-10698	Sequence 10698, A
44	40	40.8	312	9	US-09-815-242-10217	Sequence 10217, A
45	40	40.8	578	9	US-09-888-615-100	Sequence 100, App

#### ALIGNMENTS

RESULT 1

US-10-087-464-2

; Sequence 2, Application US/10087464

; Publication No. US20030059436A1

; GENERAL INFORMATION:

; APPLICANT: Chishhti, Athar

; APPLICANT: Oh, Steven

; APPLICANT: Liu, David

; APPLICANT: Goel, Vikas

; APPLICANT: Li, Xuerong

; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There

; FILE REFERENCE: S1237/7019

; CURRENT APPLICATION NUMBER: US/10/087,464

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 06/272,930

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 59

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-087-464-2

Query Match 100.0%; Score 98; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPGAA 20

DB 1 SVTHANALTMVKASTPGAA 20

RESULT 2

US-10-087-464-22

; Sequence 22, Application US/10087464

; Publication No. US20030059436A1

; GENERAL INFORMATION:

```
; APPLICANT: Chishtli, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S123777019
; CURRENT APPLICATION NUMBER: US/10/087,464
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-087-464-22

Query Match      100.0%; Score 98; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      12 SVTHANALTMVGKASTPGAA 31

RESULT 3
US-09-864-761-39328
; Sequence 39328, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
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; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: SWISSPROT HIT: P02730, EVALUE 3.00e-31
; OTHER INFORMATION: EST_HUMAN HIT: BF526005.1, EVALUE 3.00e-21
US-09-864-761-39328

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Db      45 SVTHANALTMVGKASTPGAA 64

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US-10-066-320-2
; Sequence 2, Application US/10066320
; Publication No. US20030022267A1
; GENERAL INFORMATION:
; APPLICANT: Stamler, Jonathan S.
; APPLICANT: Gow, Andrew J.
; APPLICANT: Singel, David J.
; TITLE OF INVENTION: Method for Determining Physiological
; TITLE OF INVENTION: Effects of Hemoglobin
; FILE REFERENCE: 1818.1030-003
; CURRENT APPLICATION NUMBER: US/10/066.320
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US00/21101
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US60/146,680
; PRIOR FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-320-2

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      731 SVTHANALTMVGKASTPGAA 750

RESULT 5
US-10-087-464-6
; Sequence 6, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishtli, Athar
```



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; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: SI237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-6

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Best Local Similarity 100.0%; Pred. No. 9.7e-08;
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US-10-087-464-8
; Sequence 8, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: SI237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-8

Query Match      100.0%; Score 98; DB 15; Length 911;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 731 SVTHANALTYMGKASTPGAA 750

RESULT 7
US-09-815-242-10954
; Sequence 10954, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
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; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10954
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-10954

Query Match      50.0%; Score 49; DB 9; Length 262;
Best Local Similarity 55.6%; Pred. No. 3.2;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 THANALTYMGKASTPGAA 20
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Db 175 SHANFLEVMHKSATKGA 192

RESULT 8
US-10-260-877-2
; Sequence 2, Application US/10260877
; Publication No. US20030021813A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Chovan, Linda E.
; APPLICANT: Hessler, Paul E.
; APPLICANT: Reich, Karl A.
; TITLE OF INVENTION: ESSENTIAL BACTERIA GENES AND GENOME
; TITLE OF INVENTION: SCANNING IN HAEMOPHILUS INFLUENZAE FOR THE IDENTIFICATION OF
; FILE REFERENCE: 6565.US.P1
; CURRENT APPLICATION NUMBER: US/10/260,877
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/649,145
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 262
; TYPE: PRT
; ORGANISM: H. influenzae
US-10-260-877-2

Query Match      50.0%; Score 49; DB 15; Length 262;
Best Local Similarity 55.6%; Pred. No. 3.2;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 THANALTYMGKASTPGAA 20
    :||| | | | : | | |
Db 175 SHANFLEVMHKSATKGA 192

RESULT 9
US-09-728-137-4
; Sequence 4, Application US/09728137
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RESULT 10
US-09-728-137-8
; Sequence 8, Application US/09728137
; Patent NO. US20010029031A1
; GENERAL INFORMATION:
; APPLICANT: Walter F. Boron
; APPLICANT: Antoine Michel Alain Brill
; APPLICANT: Nassirah Khandoudi
; APPLICANT: Xavier Martin
; APPLICANT: Steven Charles Jupe
; APPLICANT: Christopher John Rawlings
; APPLICANT: Trudy Rachel Doe
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30409-D1
; CURRENT APPLICATION NUMBER: US/09/728,137
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/115,954
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EP 97401714.7
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 97401713.9
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 98400272.5
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: EP 98400454.9
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.
; SEQ ID NO 8
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-728-137-8

```

```

; Sequence 4, Application US/09734674
; Patent No. US20020081649A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN
; TITLE OF INVENTION: NUCLEIC ACID
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO01018
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Vers
; SEQ ID NO 4
; LENGTH: 1085
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-734-674-4

```

Query Match 48.0%; Score 47; DB 9; Length 1085;  
Best Local Similarity 44.4%; Pred. No. 36;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPG 18  
|:|:| |:|:| :|:|  
Db 848 SITHVNSLKLESCSAPG 865

## RESULT 13

US-10-274-990-4  
; Sequence 4, Application US/10274990  
; Publication No. US20030054491A1  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CLO01018 DIV  
; CURRENT APPLICATION NUMBER: US/10/274,990  
; CURRENT FILING DATE: 2002-10-22  
; PRIOR APPLICATION NUMBER: 09/734,674  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1085  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-274-990-4

Query Match 48.0%; Score 47; DB 15; Length 1085;  
Best Local Similarity 44.4%; Pred. No. 36;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPG 18  
|:|:| |:|:| :|:|  
Db 848 SITHVNSLKLESCSAPG 865

## RESULT 14

US-09-920-804-2  
; Sequence 2, Application US/09920804  
; Patent No. US20020064846A1  
; GENERAL INFORMATION:  
; APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.  
; TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger  
; FILE REFERENCE: GP44  
; CURRENT APPLICATION NUMBER: US/09/920,804  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 2  
; LENGTH: 1088  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-920-804-2

Query Match 48.0%; Score 47; DB 9; Length 1088;  
Best Local Similarity 44.4%; Pred. No. 36;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPG 18  
|:|:| |:|:| :|:|  
Db 851 SITHVNSLKLESCSAPG 868

## RESULT 15

US-09-920-804-4  
; Sequence 4, Application US/09920804  
; Patent No. US20020064846A1  
; GENERAL INFORMATION:  
; APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.  
; TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger

; FILE REFERENCE: GP44  
; CURRENT APPLICATION NUMBER: US/09/920,804  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 8  
; SEQ ID NO 4  
; LENGTH: 1088  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-920-804-4

Query Match 48.0%; Score 47; DB 9; Length 1088;  
Best Local Similarity 44.4%; Pred. No. 36;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 SVTHANALTMVKASTPG 18  
|:|:| |:|:| :|:|  
Db 851 SITHVNSLKLESCSAPG 868

Search completed: September 3, 2003, 11:53:44  
Job time : 18.5 secs

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Result No.	Score	Match	Query	DB	ID	Description
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2	47	48.0	1032	3	US-09-115-954-8	Sequence 8, Appli
3	47	48.0	1044	3	US-09-115-954-2	Sequence 2, Appli
4	47	48.0	1085	4	US-09-734-674-4	Sequence 4, Appli
5	47	48.0	1129	4	US-09-734-674-2	Sequence 2, Appli
6	44	44.9	407	2	US-08-926-327-2	Sequence 2, Appli
7	44	44.9	407	3	US-09-119-918-2	Sequence 2, Appli
8	44	44.9	4551	3	US-09-320-878-1	Sequence 1, Appli
9	42	42.9	4551	4	US-09-141-908-2	Sequence 2, Appli
10	42	42.9	4551	4	US-09-657-440-1	Sequence 1, Appli
11	42	42.9	4613	3	US-09-105-537-31	Sequence 31, Appli
12	42	42.9	11877	3	US-09-105-537-6	Sequence 6, Appli
13	40	40.8	819	4	US-09-328-352-4650	Sequence 4650, Ap
14	40	40.8	872	1	US-08-491-357-3	Sequence 3, Appli
15	40	40.8	872	3	US-08-968-633-3	Sequence 3, Appli
16	40	40.8	872	3	US-09-196-466-3	Sequence 3, Appli
17	40	40.8	872	5	PCR-US96-10823-3	Sequence 3, Appli
18	39	39.8	208	2	US-08-700-607-7	Sequence 7, Appli
19	39	39.8	263	4	US-07-411-977-2	Sequence 2, Appli
20	39	39.8	266	2	US-07-857-224B-44	Sequence 44, Appli
21	39	39.8	297	4	US-09-252-991A-19325	Sequence 19325, A
22	39	39.8	297	4	US-08-700-607-6	Sequence 6, Appli
23	39	39.8	402	1	US-08-314-309A-6	Sequence 6, Appli
24	39	39.8	441	1	US-08-314-309A-4	Sequence 4, Appli
25	39	39.8	505	4	US-09-252-991A-23925	Sequence 23925, A
26	39	39.8	776	2	US-08-700-607-5	Sequence 5, Appli
27	39	39.8	882	4	US-09-328-352-5232	Sequence 5232, Ap

; CURRENT FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: EP97401714.7  
; EARLIER FILING DATE: 1997-07-16  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 1032  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-115-954-8

Query Match 48.0%; Score 47; DB 3; Length 1032;  
Best Local Similarity 44.4%; Pred. No. 11;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SVTHANALTMGKASTPG 18  
|:|:| |:|:| :|:|  
Db 838 SITHVNSLKLESECSAPG 855

RESULT 3  
US-09-115-954-2  
; Sequence 2, Application US/09115954B  
; Patent No. 6200776  
; GENERAL INFORMATION:  
; APPLICANT: Boron, Walter F  
; APPLICANT: Brill, Antoine M  
; APPLICANT: Khandoudi, Nassirah  
; APPLICANT: Martin, Xavier  
; APPLICANT: Jupe, Steven C  
; APPLICANT: Rawlings, Christopher J  
; APPLICANT: Doe, Trudy R  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GH-30409  
; CURRENT APPLICATION NUMBER: US/09/115.954B  
; CURRENT FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: EP97401714.7  
; EARLIER FILING DATE: 1997-07-16  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1044  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-115-954-2

Query Match 48.0%; Score 47; DB 3; Length 1044;  
Best Local Similarity 44.4%; Pred. No. 12;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SVTHANALTMGKASTPG 18  
|:|:| |:|:| :|:|  
Db 850 SITHVNSLKLESECSAPG 867

RESULT 4  
US-09-734-674-4  
; Sequence 4, Application US/09734674  
; Patent No. 6498022  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL001018  
; CURRENT APPLICATION NUMBER: US/09/734.674  
; CURRENT FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1085  
; TYPE: PRT  
; ORGANISM: Mus musculus

US-09-734-674-4

Query Match 48.0%; Score 47; DB 4; Length 1085;  
Best Local Similarity 44.4%; Pred. No. 12;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SVTHANALTMGKASTPG 18  
|:|:| |:|:| :|:|  
Db 848 SITHVNSLKLESECSAPG 865

RESULT 5  
US-09-734-674-2  
; Sequence 2, Application US/09734674  
; Patent No. 6498022  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL001018  
; CURRENT APPLICATION NUMBER: US/09/734.674  
; CURRENT FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1129  
; TYPE: PRT  
; ORGANISM: Human  
US-09-734-674-2

Query Match 48.0%; Score 47; DB 4; Length 1129;  
Best Local Similarity 44.4%; Pred. No. 13;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SVTHANALTMGKASTPG 18  
|:|:~ |:|:~ :|:|  
Db 892 SITHVNSLKLESECSAPG 909

RESULT 6  
US-08-926-327-2  
; Sequence 2, Application US/08926327  
; Patent No. 5821100  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H.  
; APPLICANT: Solenberg, Patricia J.  
; TITLE OF INVENTION: Glycosyltransferase Gene gtfB From  
; TITLE OF INVENTION: Anycolatopsis Orientalis  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: U.S.  
; ZIP: 46285  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/926.327  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Webster, Thomas D.  
; REGISTRATION NUMBER: 39,872  
; REFERENCE/DOCKET NUMBER: P-10898  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 317-276-3334  
; INFORMATION FOR SEQ ID NO: 2;

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 407 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-926-327-2

Query Match 44.9%; Score 44; DB 2; Length 407;  
Best Local Similarity 55.6%; Pred. No. 13;  
Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 THANALTMVGKASTPGAA 20  
||| | | | | | | |  
Db 371 THARATAVAGTIRTDGAA 388

## RESULT 7

US-09-119-918-2  
; Sequence 2, Application US/09119918  
; Patent No. 6025173  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H.  
; APPLICANT: Solenberg, Patricia J.  
; TITLE OF INVENTION: Glycosyltransferase Gene gtfB From  
; TITLE OF INVENTION: Anycolatopsis Orientalis  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Eli Lilly and Company  
; STREET: Lilly Corporate Center  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: U.S.  
; ZIP: 46285

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/119,918.  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/926,327  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Webster, Thomas D.  
; REGISTRATION NUMBER: 39,872  
; REFERENCE/DOCKET NUMBER: P-10898  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 317-276-3334  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 407 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-119-918-2

Query Match 44.9%; Score 44; DB 3; Length 407;  
Best Local Similarity 55.6%; Pred. No. 13;  
Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 THANALTMVGKASTPGAA 20  
||| | | | | | | |  
Db 371 THARATAVAGTIRTDGAA 388

## RESULT 8

US-09-320-878-1  
; Sequence 1, Application US/09320878A  
; Patent No. 6117659  
; GENERAL INFORMATION:

; APPLICANT: ASHLEY, Gary  
; APPLICANT: BETLACH, Melanie C.  
; APPLICANT: BETLACH, Mary C.  
; APPLICANT: MCDANIEL, Robert  
; APPLICANT: TANG, Li  
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 300622002100  
; CURRENT APPLICATION NUMBER: US/09/320,878A  
; CURRENT FILING DATE: 1999-05-27  
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
; EARLIER FILING DATE: 1998-08-28  
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
; EARLIER FILING DATE: 1998-05-06  
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
; EARLIER FILING DATE: 1997-04-30  
; EARLIER APPLICATION NUMBER: 60/119,139  
; EARLIER FILING DATE: 1999-02-08  
; EARLIER APPLICATION NUMBER: 60/100,880  
; EARLIER FILING DATE: 1998-09-22  
; EARLIER APPLICATION NUMBER: 60/087,080  
; EARLIER FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4551  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-320-878-1

Query Match 42.9%; Score 42; DB 3; Length 4551;  
Best Local Similarity 56.2%; Pred. No. 4.7e+02;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ANALTMVGKASTPGAA 20  
|:|:| | | | | | | |  
Db 4305 ASASTAGTAGTGPGA 4320

## RESULT 9

US-09-141-908-2  
; Sequence 2, Application US/09141908  
; Patent No. 6503741  
; GENERAL INFORMATION:  
; APPLICANT: ASHLEY, Gary  
; APPLICANT: BETLACH, Melanie C.  
; APPLICANT: BETLACH, Mary  
; APPLICANT: MCDANIEL, Robert  
; APPLICANT: TANG, Li  
; TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a  
; TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold  
; FILE REFERENCE: 300622002100  
; CURRENT APPLICATION NUMBER: US/09/141,908  
; CURRENT FILING DATE: 1998-08-28  
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
; EARLIER FILING DATE: 1998-05-06  
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
; EARLIER FILING DATE: 1997-04-30  
; EARLIER APPLICATION NUMBER: PROV. 60/076,919  
; EARLIER FILING DATE: 1998-03-05  
; EARLIER APPLICATION NUMBER: PROV. 60/087,080  
; EARLIER FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 4551  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-141-908-2

Query Match 42.9%; Score 42; DB 4; Length 4551;  
Best Local Similarity 56.2%; Pred. No. 4.7e+02;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ANALYMGKASTPGAA 20  
I:| | | | |  
Db 4305 ASASTTAGTAGTCTA 4320

## RESULT 10

US-09-657-440-1  
; Sequence 1, Application US/09657440  
; Patent No. 6509455  
; GENERAL INFORMATION:  
; APPLICANT: ASHLEY, Gary  
; APPLICANT: BETLACH, Melanie C.  
; APPLICANT: BETLACH, Mary C.  
; APPLICANT: MCDANIEL, Robert  
; APPLICANT: TANG, Li  
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 300622002120  
; CURRENT APPLICATION NUMBER: US/09/657,440  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR FILING DATE: 1999-05-27  
; PRIOR APPLICATION NUMBER: CIP OF 09/141,908  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4551  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-657-440-1

Query Match 42.9%; Score 42; DB 4; Length 4551;  
Best Local Similarity 56.2%; Pred. No. 4.7e+02;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ANALYMGKASTPGAA 20  
I:| | | | |  
Db 4305 ASASTTAGTAGTCTA 4320

## RESULT 11

US-09-105-537-31  
; Sequence 31, Application US/09105537A  
; Patent No. 6265202  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600.438US1  
; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 4613  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-105-537-31

Query Match 42.9%; Score 42; DB 3; Length 4613;  
Best Local Similarity 56.2%; Pred. No. 4.8e+02;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ANALYMGKASTPGAA 20  
I:| | | | |  
Db 4367 ASASTTAGTAGTCTA 4382

## RESULT 12

US-09-105-537-6  
; Sequence 6, Application US/09105537A

; Patent No. 6265202  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600.438US1  
; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 11877  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-105-537-6

Query Match 42.9%; Score 42; DB 3; Length 11877;  
Best Local Similarity 56.2%; Pred. No. 1.4e+03;  
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 ANALYMGKASTPGAA 20  
I:| | | | |  
Db 4703 ASASTTAGTAGTCTA 4718

## RESULT 13

US-09-328-352-4650  
; Sequence 4650, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GRC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4650  
; LENGTH: 819  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-4650

Query Match 40.8%; Score 40; DB 4; Length 819;  
Best Local Similarity 40.0%; Pred. No. 1.4e+02;  
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SVTHANALYMGKASTPGAA 20  
I:| | | | |  
Db 696 SIADGSALTVLGDFMPATA 715

## RESULT 14

US-08-491-357-3  
; Sequence 3, Application US/08491357  
; Patent No. 5716782  
; GENERAL INFORMATION:  
; APPLICANT: Golemis, Erica A.  
; APPLICANT: Law, Susan  
; APPLICANT: Estojak, JoAnne  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A SIGNAL  
; TITLE OF INVENTION: MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL  
; TITLE OF INVENTION: ALTERATIONS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
; STREET: 1601 Market Street Suite 720  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-2307



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/491,357  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 872 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-491-357-3

Query Match 40.8%; Score 40; DB 1; Length 872;  
Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPG 18  
| | | | | : | : | | | |  
Db 473 STTVAHLDDLVSASGPG 490

RESULT 15  
US-08-968-633-3  
Sequence 3, Application US/08968633  
Patent No. 6100384  
GENERAL INFORMATION:  
APPLICANT: Golemis, Erica A.  
APPLICANT: Law, Susan  
APPLICANT: Estojak, JoAnne  
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A SIGNAL  
TITLE OF INVENTION: MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL  
ALTERATIONS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
STREET: 1601 Market Street Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,633  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/491,357  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Janet E.  
REGISTRATION NUMBER: 36,252  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 872 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. 6100384 Relevant  
TOPOLOGY: No. 6100384 Relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-968-633-3

Query Match 40.8%; Score 40; DB 3; Length 872;  
Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPG 18  
| | | | | : | : | | | |  
Db 473 STTVAHLDDLVSASGPG 490

Search completed: September 3, 2003, 11:52:27  
Job time : 16.75 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	96	100.0	20	15	US-10-087-464-3		Sequence 3, Appli
2	96	100.0	42	15	US-10-087-464-22		Sequence 22, Appl
3	96	100.0	86	9	US-09-864-761-39328		Sequence 39328, A
4	96	100.0	911	15	US-10-066-320-2		Sequence 2, Appli
5	96	100.0	911	15	US-10-087-464-6		Sequence 6, Appli
6	96	100.0	911	15	US-10-087-464-8		Sequence 8, Appli
7	50	52.1	1317	10	US-09-963-896-7		Sequence 7, Appli
8	45	45.9	20	15	US-10-087-464-2		Sequence 2, Appli
9	44	45.8	3816	11	US-09-808-880-3		Sequence 3, Appli
10	41	42.7	114	11	US-09-764-891-3888		Sequence 3888, Ap
11	41	42.7	345	10	US-09-738-626-3894		Sequence 3894, Ap
12	41	42.7	387	14	US-10-054-5628-4		Sequence 4, Appli
13	41	42.7	473	9	US-09-790-264-39		Sequence 39, Appl
14	41	42.7	473	15	US-10-369-353-39		Sequence 39, Appl
15	40	41.7	121	10	US-09-989-920-198		Sequence 198, App

```
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S123777019
; CURRENT APPLICATION NUMBER: US/10/087,464
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-087-464-22

Query Match      100.0%; Score 96; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKASTPGAAAQIQEVKEQRI 20
        |||||
Db      23 GKASTPGAAAQIQEVKEQRI 42

RESULT 3
US-09-864-761-39328
; Sequence 39328, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39328
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003043.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: SWISSPROT HIT: P02730, EVALUE 3.00e-31
; OTHER INFORMATION: EST_HUMAN HIT: BF526005.1, EVALUE 3.00e-21
US-09-864-761-39328

Query Match      100.0%; Score 96; DB 9; Length 86;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKASTPGAAAQIQEVKEQRI 20
        |||||
Db      56 GKASTPGAAAQIQEVKEQRI 75

RESULT 4
US-10-066-320-2
; Sequence 2, Application US/10066320
; Publication No. US20030022267A1
; GENERAL INFORMATION:
; APPLICANT: Stamler, Jonathan S.
; APPLICANT: Gow, Andrew J.
; APPLICANT: Singel, David J.
; TITLE OF INVENTION: Method for Determining Physiological
; FILE REFERENCE: 1818.1030-003
; CURRENT APPLICATION NUMBER: US/10/066,320
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US00/21101
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US60/146,680
; PRIOR FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-320-2

Query Match      100.0%; Score 96; DB 15; Length 911;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKASTPGAAAQIQEVKEQRI 20
        |||||
Db      742 GKASTPGAAAQIQEVKEQRI 761

RESULT 5
US-10-087-464-6
; Sequence 6, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishtli, Athar
```

```
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-6

Query Match      100.0%; Score 96; DB 15; Length 911;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKASTPGAAQIQEVKEQRI 20
      ||||||||||||||||||
Db      742 GKASTPGAAQIQEVKEQRI 761

RESULT 6
US-10-087-464-8
; Sequence 8, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-8

Query Match      100.0%; Score 96; DB 15; Length 911;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKASTPGAAQIQEVKEQRI 20
      ||||||||||||||||||
Db      742 GKASTPGAAQIQEVKEQRI 761

RESULT 7
US-09-963-896-7
; Sequence 7, Application US/09963896
; Patent No. US20020102585A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
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; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/963,896
; FILING DATE: 26-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/397,558
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0527 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1317 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 2459993
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-963-896-7

Query Match      52.1%; Score 50; DB 10; Length 1317;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 GKASTPGAAQIQEV 15
      | |||:|||||:
Db      448 GAASSPGSAARLQEL 462

RESULT 8
US-10-087-464-2
; Sequence 2, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-2

Query Match      46.9%; Score 45; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKASTPGAA 9
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Db 12 GKSTPGAA 20  
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## RESULT 9

US-09-808-880-3  
; Sequence 3, Application US/09808880  
; Publication No. US20030027287A1  
; GENERAL INFORMATION:  
; APPLICANT: Betlach, Mary C.  
; APPLICANT: Shah, Sanjay Krishnakant  
; APPLICANT: McDaniel, Robert  
; APPLICANT: Tang, Li  
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 30062-20029.00  
; CURRENT APPLICATION NUMBER: US/09/808,880  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: US/09/428,517  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/120,254  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/106,100  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 3816  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant  
; OTHER INFORMATION: Oleandolide PKS  
US-09-808-880-3

Query Match 45.8%; Score 44; DB 11; Length 3816;  
Best Local Similarity 60.0%; Pred. No. 8.3e+02;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 STPGAAAIQIEVKQ 18  
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Db 1412 SIPGALASLQEVLDQ 1426

## RESULT 10

US-09-764-891-3888  
; Sequence 3888, Application US/09764891  
; Publication No. US20030077808A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC006  
; CURRENT APPLICATION NUMBER: US/09/764,891  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 10231  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 3888  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (88)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-891-3888

Query Match 42.7%; Score 41; DB 11; Length 114;  
Best Local Similarity 66.7%; Pred. No. 48;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KASTPGAAAIQ 13  
: | | | | | : |  
Db 16 QASTPGAAAVQ 27

## RESULT 11

US-09-738-626-3894  
; Sequence 3894, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENO, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 3894  
; LENGTH: 345  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-3894

Query Match 42.7%; Score 41; DB 10; Length 345;  
Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ASTPGAAAIQIEVKQ 18  
| | | | | : | | | | |  
Db 40 ASTDGTASRLLEKEK 55

## RESULT 12

US-10-054-562A-4  
; Sequence 4, Application US/10054562A  
; Publication No. US20020165375A1  
; GENERAL INFORMATION:  
; APPLICANT: Chandrashekar, Ramaswamy  
; APPLICANT: Morales, Tony H.  
; TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES,  
; FILE REFERENCE: HW-8-2  
; CURRENT APPLICATION NUMBER: US/10/054,562A  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 09/812,642  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: 09/323,427  
; PRIOR FILING DATE: 1999-06-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Dirofilaria immitis  
US-10-054-562A-4

Query Match 42.7%; Score 41; DB 14; Length 387;  
Best Local Similarity 44.4%; Pred. No. 1.9e+02;

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; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-269-353-39

Query Match      42.7%   Score 41; DB 15; Length 473;
Best Local Similarity 47.1%; Pred. No. 2.4e+02;
Matches      8; Conservative    4; Mismatches     5; Indels    0; Gaps    0;

QY      1 GKASTPGAAQAIOEVKE 17
        |::|::|::|::|::|

Db       292 GAASSPGSAHQNSNAIEE 308

RESULT 15
US-09-989-920-198
; Sequence 198, Application US/09989920
; Patent No. US20020172957A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DX-0291
; CURRENT APPLICATION NUMBER: US/09/989,920
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,500
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 198
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-920-198

Query Match      41.7%   Score 40; DB 10; Length 121;
Best Local Similarity 40.0%; Pred. No. 73;
Matches      6; Conservative    6; Mismatches     3; Indels    0; Gaps    0;

QY      1 GKASTPGAAQAIOEV 15
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Db       29 GSSSPASASQVAEI 43

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Job time : 17.5 secs
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Search completed: September 3, 2003, 11:53:44  
Job time : 17.5 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:42:58 ; Search time 15.75 seconds  
(without alignments)  
53.728 Million cell updates/sec

Title: US-10-087-464-3  
Perfect score: 96  
Sequence: 1 GKASTPGAAQIQEVKEQRI 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*  
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6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	52.1	1317	3 US-09-083-521-7	Sequence 7, Appli
2	45	46.9	577	4 US-09-252-991A-32531	Sequence 32531, A
3	44.5	46.4	490	4 US-09-252-991A-22504	Sequence 22504, A
4	44	45.8	3816	3 US-09-428-517-3	Sequence 3, Appli
5	42	43.8	286	4 US-09-252-991A-31069	Sequence 31069, A
6	42	43.8	343	4 US-09-252-991A-24458	Sequence 24458, A
7	42	43.8	362	4 US-09-252-991A-30223	Sequence 30223, A
8	41	42.7	387	3 US-09-323-427-4	Sequence 4, Appli
9	41	42.7	387	4 US-08-812-642-4	Sequence 4, Appli
10	41	42.7	827	3 US-08-669-286-11	Sequence 11, Appl
11	41	42.7	827	3 US-09-469-253-11	Sequence 11, Appl
12	41	42.7	827	3 US-09-642-146-11	Sequence 11, Appl
13	40.5	42.2	460	4 US-09-252-991A-18921	Sequence 18921, A
14	40	41.7	137	4 US-09-107-532A-3757	Sequence 3757, Ap
15	40	41.7	144	3 US-09-319-989-4	Sequence 4, Appli
16	40	41.7	334	4 US-09-198-452A-70	Sequence 70, Appl
17	40	41.7	848	3 US-08-976-255-10	Sequence 10, Appl
18	39	40.6	94	4 US-09-442-099A-11	Sequence 11, Appl
19	39	40.6	94	4 US-09-612-342-11	Sequence 11, Appl
20	39	40.6	120	4 US-09-442-099A-12	Sequence 12, Appl
21	39	40.6	120	4 US-09-612-342-12	Sequence 12, Appl
22	39	40.6	181	4 US-09-442-099A-10	Sequence 10, Appl
23	39	40.6	181	4 US-09-612-342-10	Sequence 10, Appl
24	39	40.6	185	4 US-09-513-057C-19	Sequence 19, Appl
25	39	40.6	306	4 US-09-252-991A-30395	Sequence 30395, A
26	39	40.6	327	4 US-09-252-991A-21037	Sequence 21037, A
27	39	40.6	451	4 US-09-252-991A-31986	Sequence 31986, A

28	39	40.6	545	4 US-09-269-731-8	Sequence 8, Appli
29	39	40.6	620	4 US-09-252-991A-20833	Sequence 20833, A
30	39	40.6	639	4 US-09-252-991A-23693	Sequence 23693, A
31	39	40.6	704	4 US-09-252-991A-22320	Sequence 22320, A
32	38.5	40.1	937	4 US-09-252-991A-32336	Sequence 32336, A
33	38	39.6	89	4 US-09-252-991A-18394	Sequence 18394, A
34	38	39.6	239	3 US-09-479-309-2	Sequence 2, Appli
35	38	39.6	239	4 US-09-627-393-2	Sequence 2, Appli
36	38	39.6	282	4 US-09-252-991A-32829	Sequence 32829, A
37	38	39.6	330	4 US-09-252-991A-31292	Sequence 31292, A
38	38	39.6	394	4 US-09-252-991A-28148	Sequence 28148, A
39	38	39.6	400	4 US-09-252-991A-29728	Sequence 29728, A
40	38	39.6	416	4 US-08-978-289-12	Sequence 12, Appl
41	38	39.6	416	4 US-09-601-478-1	Sequence 1, Appli
42	38	39.6	416	4 US-09-601-478-4	Sequence 4, Appli
43	38	39.6	570	4 US-09-252-991A-27338	Sequence 27338, A
44	38	39.6	728	4 US-09-252-991A-28169	Sequence 28169, A
45	38	39.6	782	4 US-09-252-991A-20548	Sequence 20548, A

ALIGNMENTS

RESULT 1  
US-09-083-521-7  
; Sequence 7, Application US/09083521  
; Patent No. 6048970  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Guegler, Karl J.  
; TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/083,521  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CERRONE, MICHAEL C.  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PF-0527 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1317 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 2459993  
US-09-083-521-7

Query Match 52.1%; Score 50; DB 3; Length 1317;  
Best Local Similarity 60.0%; Pred. No. 8.9;  
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GKASTPGAAQIQEV 15  
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Db      448 GAASSPGSAARLQEL 462

RESULT 2
US-09-252-991A-32531
; Sequence 32531, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32531
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32531

Query Match      46.9%; Score 45; DB 4; Length 577;
Best Local Similarity 52.9%; Pred. No. 23;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      2 KASTPGAAAOIQEVKEQ 18
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Db      191 QASTHGADAEIQPLEREQ 207

RESULT 3
US-09-252-991A-22504
; Sequence 22504, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22504
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22504

Query Match      46.4%; Score 44.5; DB 4; Length 490;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 9; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Qy      1 GKASTPGAAAOIQEVKEQ 18
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Db      94 GRADQPG-AAEVQOVRQ 110

RESULT 4
US-09-428-517-3
; Sequence 3, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
; APPLICANT: Betlach, Mary C.
; APPLICANT: Shah, Sanjay Krishnakant
; APPLICANT: McDaniel, Robert

```

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; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428.517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3816
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-3

Query Match      45.8%; Score 44; DB 3; Length 3816;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      4 STPGAAAOIQEVKEQ 18
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Db      1412 SIPGALASLQEVLDQ 1426

RESULT 5
US-09-252-991A-31069
; Sequence 31069, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31069
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31069

Query Match      43.8%; Score 42; DB 4; Length 286;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      5 TPGAAAOIQEVKEQRI 20
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Db      206 TPGAAVQLHGEEQAV 221

RESULT 6
US-09-252-991A-24458
; Sequence 24458, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

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TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:

US-09-642-146-11  
; Sequence 11, Application US/09642146

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; LENGTH: 460
;
; TYPE: PRT
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; ORGANISM: Pseudomonas aeruginosa
;
; FEATURE:
;
; NAME/KEY: UNSURE
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; LOCATION: (252),(292)  
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
US-09-252-991A-18921

Query Match 42.2%; Score 40.5; DB 4; Length 460;  
Best Local Similarity 45.0%; Pred. No. 97;  
Matches 9; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Qy 1 GKASTPGAAAIQ-EVKEQR 19  
Db 193 GRDAPGASGEVQEEVEQR 212

## RESULT 14

US-09-107-532A-3757  
; Sequence 3757, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354

COMPUTER READABLE FORM:  
MEDIUM TYPE: CD/ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3757:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:

NAME/KEY: misc\_feature  
LOCATION: (B) LOCATION 1...137  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3757:  
US-09-107-532A-3757

Query Match 41.7%; Score 40; DB 4; Length 137;  
Best Local Similarity 36.8%; Pred. No. 30;  
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 2 KASTPGAAAIQ-EVKEQRI 20  
Db 7 KMSSPGVPLDLSLKEKI 25

## RESULT 15

US-09-319-989-4  
; Sequence 4, Application US/09319989  
; Patent No. 6190914  
; GENERAL INFORMATION:

; APPLICANT: Grivell, Leslie A.  
; APPLICANT: Teixeira De Mattos, Maarten J.  
; APPLICANT: Blom, Jolanda

; TITLE OF INVENTION: METHODS FOR MODULATING METABOLIC PATHWAYS OF  
; MICRO-ORGANISMS AND MICRO-ORGANISMS OBTAINABLE BY SAID  
; TITLE OF INVENTION: METHODS

; FILE REFERENCE: 24615-20123.00  
; CURRENT APPLICATION NUMBER: US/09/319,989  
; CURRENT FILING DATE: 1999-06-14  
; EARLIER APPLICATION NUMBER: PCT/NL97/00688  
; EARLIER FILING DATE: 1997-12-12  
; EARLIER APPLICATION NUMBER: EPO 96203520  
; EARLIER FILING DATE: 1996-12-12  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 144

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: HAP3  
US-09-319-989-4

Query Match 41.7%; Score 40; DB 3; Length 144;  
Best Local Similarity 44.4%; Pred. No. 31;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GKASTPGAAAIQ-EVKEQ 18  
Db 21 GNASSGSLQIISTLREQ 38

Search completed: September 3, 2003, 11:52:29  
Job time : 17.75 secs

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2	112	100.0	51	15	US-10-087-464-23		Sequence 23, Appli
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4	112	100.0	911	15	US-10-087-464-6		Sequence 6, Appli
5	112	100.0	911	15	US-10-087-464-8		Sequence 8, Appli
6	62	55.4	56	9	US-09-864-761-34894		Sequence 34894, A
7	52	46.4	336	9	US-09-747-804-1		Sequence 1, Appli
8	50	44.6	542	10	US-09-908-805B-44		Sequence 44, Appli
9	49	43.8	1088	9	US-09-920-804-2		Sequence 2, Appli
10	49	43.8	1088	9	US-09-920-804-4		Sequence 4, Appli
11	49	43.8	1129	9	US-09-734-674-2		Sequence 2, Appli
12	49	43.8	1129	15	US-10-274-990-2		Sequence 2, Appli
13	48	42.9	1035	15	US-10-205-823-373		Sequence 373, App
14	46	41.1	578	9	US-09-732-020-2		Sequence 2, Appli
15	45	40.2	186	9	US-09-811-284-176		Sequence 176, App

```
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-087-464-23

Query Match          100.0%; Score 112; DB 15; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DRILLFKPKYHPDVPYK 20

RESULT 3
US-10-066-320-2
; Sequence 2, Application US/10066320
; Publication No. US2003002267A1
; GENERAL INFORMATION:
; APPLICANT: Stamler, Jonathan S.
; APPLICANT: Gow, Andrew J.
; APPLICANT: Singel, David J.
; TITLE OF INVENTION: Method for Determining Physiological
; TITLE OF INVENTION: Effects of Hemoglobin
; FILE REFERENCE: 1818.1030-003
; CURRENT APPLICATION NUMBER: US/10/066,320
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: PCT/US00/21101
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US60/146,680
; PRIOR FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-320-2

Query Match          100.0%; Score 112; DB 15; Length 911;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRILLFKPKYHPDVPYK 20
Db 807 DRILLFKPKYHPDVPYK 826

RESULT 4
US-10-087-464-6
; Sequence 6, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
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; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-6

Query Match          100.0%; Score 112; DB 15; Length 911;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRILLFKPKYHPDVPYK 20
Db 807 DRILLFKPKYHPDVPYK 826

RESULT 5
US-10-087-464-8
; Sequence 8, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-8

Query Match          100.0%; Score 112; DB 15; Length 911;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRILLFKPKYHPDVPYK 20
Db 807 DRILLFKPKYHPDVPYK 826

RESULT 6
US-09-864-761-34894
; Sequence 34894, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 34894  
; LENGTH: 56  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC009955.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1  
; OTHER INFORMATION: EST\_HUMAN HIT: BE868202.1, EVALUE 3.00e-16  
; OTHER INFORMATION: SWISSPROT HIT: O18917, EVALUE 1.00e-25  
US-09-864-761-34894

Query Match 55.4%; Score 62; DB 9; Length 56;  
Best Local Similarity 55.6%; Pred. No. 0.047;  
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 RILLFKPKYHPDPVYV 19  
|:|:| | |:|:| | |  
Db 37 RLLILMPAKHHPQYV 54

RESULT 7  
US-09-747-804-1  
; Sequence 1, Application US/09747804  
; Patent No. US20010010913A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Patterson, Chandra

; TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS  
; FILE REFERENCE: PF-0576 US  
; CURRENT APPLICATION NUMBER: US/09/747,804  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 09/131,648  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 336  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 2635136  
US-09-747-804-1

Query Match 46.4%; Score 52; DB 9; Length 336;  
Best Local Similarity 57.1%; Pred. No. 8.6;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LFKPKYHPDPVYV 19  
: | | : | | | | |  
Db 37 ILQPPVHPVYV 50

RESULT 8  
US-09-805B-44  
; Sequence 44, Application US/09908805B  
; Patent No. US20020147307A1  
; GENERAL INFORMATION:  
; APPLICANT: HILTON, Douglas J  
; APPLICANT: ALEXANDER, Warren S  
; APPLICANT: VINEY, Elizabeth M  
; APPLICANT: WILLSON, Tracey A  
; APPLICANT: RICHARDSON, Rachael T  
; APPLICANT: STARR, Robyn  
; APPLICANT: NICHOLSON, Sandra E  
; APPLICANT: METCALF, Donald  
; APPLICANT: NICOLA, Nicos A  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS  
; FILE REFERENCE: 109762  
; CURRENT APPLICATION NUMBER: US/09/908,805B  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 08/962,560  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 81  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 542  
; TYPE: PRT  
; ORGANISM: Mouse  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (94)  
; OTHER INFORMATION: Xaa is unsure  
US-09-908-805B-44

Query Match 44.6%; Score 50; DB 10; Length 542;  
Best Local Similarity 47.4%; Pred. No. 28;  
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDPVYV 19  
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Db 356 EEILQLEAPKFKHTQIDYV 374

RESULT 9  
US-09-920-804-2  
; Sequence 2, Application US/09920804  
; Patent No. US20020064846A1  
; GENERAL INFORMATION:  
; APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.  
; TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger

Query Match 42.9%; Score 48; DB 15; Length 1035;

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Best Local Similarity 45.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;
Matches 9; Conservative 4; Mismatches 7;

QY 1 DRILLFKPKYHPDVPYVK 20
Db 880 DRKLKLLMLPKHPDFIYLR 899

RESULT 14
US-09-732-020-2
; Sequence 2, Application US/09732020
; Patent No. US20010003743A1
; GENERAL INFORMATION:
; APPLICANT: Henrik, Olsen
; APPLICANT: Timothy, Coleman
; APPLICANT: Mark, Adams
; TITLE OF INVENTION: Human Oxalyl-CoA Decarboxylase
; FILE REFERENCE: PF119D3
; CURRENT APPLICATION NUMBER: US/09/732,020
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/326,217
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 08/867,970
; PRIOR FILING DATE: 1997-06-03
; PRIOR APPLICATION NUMBER: 08/458,120
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/US94/05561
; PRIOR FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 578
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-732-020-2

Query Match 41.1%; Score 46; DB 9; Length 578;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 PKKYHPDVPYVK 20
Db 292 PPRYQPDVKFIQ 303

RESULT 15
US-09-811-284-176
; Sequence 176, Application US/09811284
; Patent No. US20020058306A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US20020058306A1e1 G Protein-Coupled Receptors
; FILE REFERENCE: 00167US1
; CURRENT APPLICATION NUMBER: US/09/811,284
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,783
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,907
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,918
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,960
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/189,917
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/192,945
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,916
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,923
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,933
; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: 60/192,830
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/192,234
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/192,155
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,935
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 176
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-284-176

Query Match 40.2%; Score 45; DB 9; Length 186;
Best Local Similarity 61.5%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 KPPKYHPDVPYVK 20
Db 156 KPPKAKPDPILK 168

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Job time : 18.5 secs
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:42:58 ; Search time 15.75 seconds  
(without alignments)  
53.728 Million cell updates/sec

Title: US-10-087-464-4

Perfect score: 112

Sequence: 1 DRILLFPKPKYHPDPVYK 20

Scoring table: BLOSUM62

Gapex 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA.\*  
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4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pap.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pap.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	112	100.0	58	US-08-405-647B-43	Sequence 43, Appl
2	112	100.0	58	US-08-985-499-43	Sequence 43, Appl
3	112	100.0	58	PCT-US96-03180-43	Sequence 43, Appl
4	79	70.5	14	US-08-405-647B-9	Sequence 9, Appl
5	79	70.5	14	US-08-985-499-9	Sequence 9, Appl
6	79	70.5	14	PCT-US96-03180-9	Sequence 9, Appl
7	69	61.6	11	US-08-269-441A-15	Sequence 15, Appl
8	52	46.4	336	US-09-131-648-1	Sequence 1, Appl
9	50	44.6	119	US-09-012-504A-24	Sequence 24, Appl
10	50	44.6	542	US-09-302-769-44	Sequence 44, Appl
11	49	43.8	1129	US-09-734-674-2	Sequence 2, Appl
12	48	42.9	376	US-08-666-367B-8	Sequence 8, Appl
13	48	42.9	376	US-09-143-438-8	Sequence 8, Appl
14	48	42.9	1079	US-09-136-652-2	Sequence 2, Appl
15	47.5	42.4	169	US-08-476-509B-28	Sequence 28, Appl
16	46.5	41.5	147	US-08-464-342-2	Sequence 2, Appl
17	46.5	41.5	147	US-08-464-604A-2	Sequence 2, Appl
18	46.5	41.5	147	US-08-875-272-2	Sequence 2, Appl
19	46.5	41.5	147	US-08-903-396-2	Sequence 2, Appl
20	46	41.1	7	US-08-405-647B-14	Sequence 14, Appl
21	46	41.1	7	US-08-985-499-14	Sequence 14, Appl
22	46	41.1	7	PCT-US96-03180-14	Sequence 14, Appl
23	46	41.1	578	US-08-458-120-2	Sequence 2, Appl
24	46	41.1	578	US-08-867-970-2	Sequence 2, Appl
25	46	41.1	578	US-09-326-217-2	Sequence 2, Appl
26	46	41.1	578	US-09-732-020-2	Sequence 2, Appl
27	45	40.2	340	US-08-102-385G-18	Sequence 18, Appl

28 45 40.2 406 1 US-08-446-777-4 Sequence 4, Appl  
29 45 40.2 767 1 US-08-446-777-6 Sequence 6, Appl  
30 45 40.2 767 1 US-08-446-777-8 Sequence 8, Appl  
31 43.5 38.8 162 2 US-08-464-604A-8 Sequence 8, Appl  
32 43 38.4 97 4 US-09-795-926-18 Sequence 18, Appl  
33 43 38.4 147 2 US-08-647-960-7 Sequence 7, Appl  
34 43 38.4 148 4 US-09-795-926-8 Sequence 8, Appl  
35 43 38.4 186 4 US-09-795-926-12 Sequence 12, Appl  
36 43 38.4 214 4 US-09-795-926-16 Sequence 16, Appl  
37 43 38.4 265 4 US-09-795-926-6 Sequence 6, Appl  
38 43 38.4 303 4 US-09-795-926-2 Sequence 2, Appl  
39 43 38.4 324 3 US-08-946-914-11 Sequence 11, Appl  
40 43 38.4 324 4 US-09-656-450-11 Sequence 11, Appl  
41 43 38.4 393 2 US-08-467-948A-4 Sequence 4, Appl  
42 43 38.4 393 3 US-08-467-947A-4 Sequence 4, Appl  
43 43 38.4 714 3 US-09-115-954-4 Sequence 4, Appl  
44 43 38.4 1032 3 US-09-115-954-8 Sequence 8, Appl  
45 43 38.4 1044 3 US-09-115-954-2 Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-405-647B-43  
; Sequence 43, Application US/08405647B  
; Patent No. 6124262  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, Irwin W.  
; APPLICANT: Crandall, Ian E.  
; APPLICANT: Sholet, Stephen B.  
; APPLICANT: Thevenin, Bernard Jean-Marie  
; TITLE OF INVENTION: Compositions and Methods for Reducing Adhesiveness of Defective Red Blood Cells  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/405,647B  
; FILING DATE: 17-MAR-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 02307E-06870005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 58 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-405-647B-43

Query Match 100.0%; Score 112; DB 3; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFPKPKYHPDPVYK 20  
|||||

Db 8 DRILLFKPKYHPDVPYK 27

## RESULT 2

US-08-985-499-43  
Sequence 43, Application US/08985499  
Patent No. 6191103  
GENERAL INFORMATION:  
APPLICANT: Shohet, Stephen B.  
APPLICANT: Sherman, Irwin  
APPLICANT: von Adrian, Ulrich  
TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a  
TITLE OF INVENTION: Mammal  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,499  
FILING DATE: 05-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hyman, Laurence J.  
REGISTRATION NUMBER: 35,551  
REFERENCE/DOCKET NUMBER: 02307E-08450005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-985-499-43

Query Match 100.0%; Score 112; DB 3; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRILLFKPKYHPDVPYK 20

Db 8 DRILLFKPKYHPDVPYK 27

## RESULT 3

PCT-US96-03180-43  
Sequence 43, Application PC/TUS9603180  
GENERAL INFORMATION:  
APPLICANT: The Regents of the University  
APPLICANT: of California  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING  
TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Robbins, Berliner & Carson  
STREET: 201 North Figueroa Street, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90012-2628  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03180  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Berliner, Robert  
REGISTRATION NUMBER: 20,121  
REFERENCE/DOCKET NUMBER: 5555-370  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 58 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US96-03180-43

Query Match 100.0%; Score 112; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.1e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DRILLFKPKYHPDVPYK 20

Db 8 DRILLFKPKYHPDVPYK 27

## RESULT 4

US-08-405-647B-9  
Sequence 9, Application US/08405647B  
Patent No. 6124262  
GENERAL INFORMATION:  
APPLICANT: Sherman, Irwin W.  
APPLICANT: Crandall, Ian E.  
APPLICANT: Sholet, Stephen B.  
APPLICANT: Thevenin, Bernard Jean-Marie  
TITLE OF INVENTION: Compositions and Methods for Reducing  
TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/405,647B  
FILING DATE: 17-MAR-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 02307E-06870005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-405-647B-9

Query Match 70.5%; Score 79; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPPKYHPDVPYVK 20  
| | | | | | | | | |  
Db 1 KPPKYHPDVPYVK 13

## RESULT 5

US-08-985-499-9  
; Sequence 9, Application US/08985499  
; Patent No. 6191103  
; GENERAL INFORMATION:  
; APPLICANT: Shohet, Stephen B.  
; APPLICANT: Sherman, Irwin  
; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a  
; TITLE OF INVENTION: Mammal  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,499  
FILING DATE: 05-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hyman, Laurence J.

REGISTRATION NUMBER: 35,551  
REFERENCE/DOCKET NUMBER: 02307E-084500US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-985-499-9

Query Match 70.5%; Score 79; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPPKYHPDVPYVK 20  
| | | | | | | | | |  
Db 1 KPPKYHPDVPYVK 13

## RESULT 6

PCT-US96-03180-9  
; Sequence 9, Application PC/TUS9603180  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of the University  
; APPLICANT: of California  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING  
; TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Robbins, Berliner & Carson  
STREET: 201 North Figueroa Street, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90012-2628  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03180  
FILING DATE:  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Berliner, Robert  
REGISTRATION NUMBER: 20,121  
REFERENCE/DOCKET NUMBER: 5555-370  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US96-03180-9

Query Match 70.5%; Score 79; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPPKYHPDVPYVK 20  
| | | | | | | | | |  
Db 1 KPPKYHPDVPYVK 13

## RESULT 7

US-08-269-441A-15  
; Sequence 15, Application US/08269441A  
; Patent No. 5552529  
; GENERAL INFORMATION:  
; APPLICANT: Rearden, Ann  
; TITLE OF INVENTION: A NOVEL AUTOANTIGEN, PINCH  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/269,441A  
FILING DATE: 30-JUN-1994  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Halle Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07257/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
US-08-269-441A-15

Query Match          61.6%; Score 69; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FKPKYHPDVP 17
Db 1 FKPKYHPDVP 11

RESULT 8
US-09-131-648-1
; Sequence 1, Application US/09131648
; Patent No. 6168920
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
; FILE REFERENCE: PF-0576 US
; CURRENT APPLICATION NUMBER: US/09/131.648
; CURRENT FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 2635136
US-09-131-648-1

Query Match          46.4%; Score 52; DB 3; Length 336;
Best Local Similarity 57.1%; Pred. No. 1.9;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 LFKPKYHPDVPYV 19
Db 37 ILQPPVFPVVPYV 50

RESULT 9
US-09-012-504A-24
; Sequence 24, Application US/09012504A
; Patent No. 6464974
; GENERAL INFORMATION:
; APPLICANT: Berlin, V.
; APPLICANT: Chiu, I.
; APPLICANT: Cottarel, G.
; APPLICANT: Damagnez, V.
; TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
; FILE REFERENCE: APBI-P05-036
; CURRENT APPLICATION NUMBER: US/09/012.504A
; CURRENT FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: 08/360,144
; PRIOR FILING DATE: 1994-12-20
; PRIOR APPLICATION NUMBER: 08/250,795
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 119
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (103)..(103)
; OTHER INFORMATION: The 'Xaa' at location 103 stands for Asp, Gly, Ala, or Val.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(662)
; OTHER INFORMATION: n=a, c, g, or t
US-09-012-504A-24

Query Match          44.6%; Score 50; DB 4; Length 119;
Best Local Similarity 53.3%; Pred. No. 1.2;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RILLLFKPKYHPDV 16
Db 71 RMLFKFEPPLFHPNV 85

RESULT 10
US-09-302-769-44
; Sequence 44, Application US/09302769
; Patent No. 6323317
; GENERAL INFORMATION:
; APPLICANT: HILTON, Douglas J
; APPLICANT: ALEXANDER, Warren S
; APPLICANT: VINEY, Elizabeth M
; APPLICANT: WILLSON, Tracey A
; APPLICANT: RICHARDSON, Rachael T
; APPLICANT: STARR, Robyn
; APPLICANT: NICHOLSON, Sandra E
; APPLICANT: METCALF, Donald
; APPLICANT: NICOLA, Nicos A
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
; FILE REFERENCE: 109762
; CURRENT APPLICATION NUMBER: US/09/302.769
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 08/962,560
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 44
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (94)
; OTHER INFORMATION: Xaa is unsure
US-09-302-769-44

Query Match          44.6%; Score 50; DB 4; Length 542;
Best Local Similarity 47.4%; Pred. No. 6.7;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DRILLFKPKYHPDVYV 19
Db 356 EEILQLEAPPKFTQIDYV 374

RESULT 11
US-09-734-674-2
; Sequence 2, Application US/09734674
; Patent No. 6498022
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001018
; CURRENT APPLICATION NUMBER: US/09/734,674
; CURRENT FILING DATE: 2000-12-13
```



; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1129  
; TYPE: PRT  
; ORGANISM: Human  
US-09-734-674-2

Query Match 43.8%; Score 49; DB 4; Length 1129;  
Best Local Similarity 45.0%; Pred. No. 22;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDPVYK 20  
||| : | | : ||  
Db 968 DRIKFWMPAKHQPDFIVLR 987

## RESULT 12

US-08-666-367B-8  
; Sequence 8, Application US/08666367B  
; Patent No. 5854042  
; GENERAL INFORMATION:  
; APPLICANT: Shuichi TSUII et al.  
; TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/666,367B  
FILING DATE: August 19, 1996

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: mouse

US-08-666-367B-8

Query Match 42.9%; Score 48; DB 2; Length 376;  
Best Local Similarity 53.3%; Pred. No. 9.1;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 ILLLFKPKYHPDPV 17  
||| : | | : ||  
Db 223 ILLWDPSPVYHADIP 237

## RESULT 13

US-09-143-438-8  
; Sequence 8, Application US/09143438  
; Patent No. 6218161  
; GENERAL INFORMATION:  
; APPLICANT: Shuichi TSUII et al.  
; TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., #800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/143,438  
FILING DATE: August 28, 1998

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/666,367

FILING DATE: August 19, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250

TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

ORIGINAL SOURCE:  
ORGANISM: mouse

US-09-143-438-8

Query Match 42.9%; Score 48; DB 3; Length 376;  
Best Local Similarity 53.3%; Pred. No. 9.1;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 ILLLFKPKYHPDPV 17  
||| : | | : ||  
Db 223 ILLWDPSPVYHADIP 237

## RESULT 14

US-09-136-652-2  
; Sequence 2, Application US/09136652A  
; Patent No. 6096517  
; GENERAL INFORMATION:  
; APPLICANT: BRILL, ANTOINE  
; APPLICANT: KHANDOUJI, NASSIRAH  
; APPLICANT: MARTIN, XAVIER  
; APPLICANT: BORON, WALTER

TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP-30010

CURRENT APPLICATION NUMBER: US/09/136,652A  
CURRENT FILING DATE: 1998-08-19

EARLIER APPLICATION NUMBER: EP 974019473.3  
EARLIER FILING DATE: 1997-08-19

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2

LENGTH: 1079

```
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-136-652-2

Query Match      42.9%; Score 48; DB 3; Length 1079;
Best Local Similarity 45.0%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRILLFKPPKYHPDPVYVK 20
   ||: || | | | | | | | |
Db 924 DRLKLLMLPKHQDPFIYLR 943

RESULT 15
US-08-476-509B-28
; Sequence 28, Application US/08476509B
; Patent No. 6034212
; GENERAL INFORMATION:
; APPLICANT: SUDOL, MARIUS
; APPLICANT: PEER, BORK
; APPLICANT: HENRY, CHEN
; TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
; TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
; TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476.509B
; FILING DATE: 01-DEC-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-101 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-476-509B-28

Query Match      42.4%; Score 47.5; DB 3; Length 169;
Best Local Similarity 47.6%; Pred. No. 4.4;
Matches 10; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

QY 2 RILLFKPPKY-----HPDVP 17
   | | | | | | | | | |
Db 16 RLLSAFKPPAYEDVHHPTGP 36

Search completed: September 3, 2003, 11:52:29
Job time : 15.75 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:41:03 ; Search time 17.25 seconds  
(without alignments)  
111.500 Million cell updates/sec

Title: US-10-087-464-1  
Perfect score: 104  
Sequence: 1 GMPWLSATTVRSVTHANALT 20  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	848	2 A33810	band 3 anion trans
2	104	100.0	911	1 B3HU	band 3 anion trans
3	104	100.0	929	2 A25314	band 3 protein - m
4	100	96.2	844	2 I50159	anion transporter
5	100	96.2	922	2 A30816	band 3 anion trans
6	95	91.3	912	2 S59861	band 3 anion trans
7	95	91.3	918	2 S24318	band 3 anion trans
8	93	89.4	865	2 A25104	band 3 protein, no
9	93	89.4	1234	2 A34911	band 3-related pro
10	93	89.4	1237	2 A31789	band 3-related pro
11	93	89.4	1237	2 A56764	band 3-related pro
12	93	89.4	1240	2 S21086	anion exchange pro
13	89	85.6	1030	2 A42497	anion exchanger 3,
14	89	85.6	1227	2 B34911	band 3-related pro
15	89	85.6	1227	2 A33638	erythrocyte anion
16	89	85.6	1232	2 I38496	anion exchanger 3
17	84	80.8	357	2 S31828	band 3 anion trans
18	53	51.0	826	2 T28858	hypothetical prote
19	48	46.2	314	2 T44895	probable lipolic ac
20	47	45.2	1035	2 T31336	sodium bicarbonate
21	47	45.2	1035	2 T13962	sodium bicarbonate
22	47	45.2	1035	2 T14110	sodium bicarbonate
23	47	45.2	1079	2 PC7034	Na+ bicarbonate co
24	47	45.2	1079	2 T14031	sodium bicarbonate
25	46	44.2	156	2 C72506	hypothetical prote
26	45	43.3	111	2 B72722	hypothetical prote
27	45	43.3	302	2 F69000	cobalamin biosynth
28	45	43.3	727	2 A56879	diacylglycerol kin
29	45	43.3	1119	2 T37460	probable sodium bi

30 45 43.3 1175 2 T22491 hypothetical prote  
31 44 42.3 449 2 H70526 probable cytochrom  
32 44 42.3 1508 2 T27828 hypothetical prote  
33 44 42.3 1519 2 T27829 hypothetical prote  
34 43 41.3 115 2 T11840 NADH2 dehydrogenas  
35 43 41.3 305 2 D83699 hypothetical prote  
36 43 41.3 311 2 C70787 probable lipolic ac  
37 43 41.3 387 2 T22841 hypothetical prote  
38 43 41.3 415 2 T42379 PH085-like protein  
39 43 41.3 431 1 UKHU u-plasminogen acti  
40 42.5 40.9 552 1 E57987 cytochrome c-type  
41 42.5 40.9 552 2 D86101 hypothetical prote  
42 42.5 40.9 552 2 H91260 cytochrome c-type  
43 42 40.4 332 2 T45065 iron binding prote  
44 42 40.4 350 2 D83563 hypothetical prote  
45 42 40.4 354 1 MMECPW glycine betaine/L-

ALIGNMENTS

RESULT 1

A33810 band 3 anion transport protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Aug-1999  
C:Accession: A33810  
R:Kudrycki, K.E.; Shull, G.E.  
J. Biol. Chem. 264, 8185-8192, 1989  
A:Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr  
A:Reference number: A33810; MUID:8925254; PMID:2722777  
A:Accession: A33810  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-848 <KUD>  
A:Cross-references: GB:J04793; NID:g203092; PIDN:AAA0800.1; PID:g203093  
C:Superfamily: band 3 anion transport protein  
C:Keywords: alternative splicing; transmembrane protein

Query Match 100.0%; Score 104; DB 2; Length 848;  
Best Local Similarity 100.0%; Pred.No. 8.3e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
|||||  
DB 657 GMPWLSATTVRSVTHANALT 676

RESULT 2

B3HU band 3 anion transport protein, erythrocyte - human  
N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha  
C:Species: Homo sapiens (man)  
C>Date: 03-Aug-1984 #sequence\_revision 03-Oct-1995 #text\_change 22-Jun-1999  
C:Accession: A36218; S03074; I39409; A92237; A26507; A92430; A90323; A28079;  
R:Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989  
A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange  
A:Reference number: A36218; MUID:90083213; PMID:2594752  
A:Accession: A36218  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-911 <LUX>  
A:Cross-references: GB:M27819; NID:gl78215; PIDN:AAA35514.1; PID:gl78216  
R:anner, M.J.A.; Martin, P.G.; High, S.  
Biochem. J. 256, 703-712, 1988  
A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra  
A:Reference number: S03074; MUID:89134172; PMID:3223947  
A:Accession: S03074  
A:Molecule type: mRNA  
A:Residues: 1-55, 'E', 57-911 <TAN>  
A:Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714  
R:Showe, L.C.; Ballantine, M.; Huebner, K.

Genomics 1, 71-76, 1987  
A:Title: Localization of the gene for the erythroid anion exchange protein, band 3 (EMPE)  
A:Reference number: 139408; MUID:88031311; PMID:3478298  
A:Accession: 139408  
A:Molecule type: DNA  
A:Residues: 37-56 <SHO1>  
A:Cross-references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220  
A:Accession: 139409  
A:Molecule type: DNA  
A:Residues: 118-161 <SHO2>  
A:Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g553169  
R:Drickamer, L.K.  
J. Biol. Chem. 253, 7242-7248, 1978  
A:Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Identif  
A:Reference number: A92237; MUID:79027186; PMID:701248  
A:Accession: A92237  
A:Molecule type: protein  
A:Residues: 1-3 <DRI>  
R:Mawby, W.J.; Findlay, J.B.C.  
Biochem. J. 205, 465-475, 1982  
A:Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-bin  
A:Reference number: A26507; MUID:83074521; PMID:7150226  
A:Accession: A26507  
A:Molecule type: protein  
A:Residues: 437-473; 360-364, 'D', 366-369 <WAW>  
R:Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.  
J. Biol. Chem. 258, 7981-7990, 1983  
A:Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte  
A:Reference number: A92430; MUID:83238395; PMID:6345535  
A:Accession: A92430  
A:Molecule type: protein  
A:Residues: 1-10, 'D', 12-68, 'E', 69-200 <KAW>  
R:Brock, C.J.; Tanner, M.J.A.; Kempf, C.  
Biochem. J. 213, 577-586, 1983  
A:Title: The human erythrocyte anion-transport protein.  
A:Reference number: A90323; MUID:83308584; PMID:6615451  
A:Accession: A90323  
A:Molecule type: protein  
A:Residues: 559-630 <BRO>  
R:Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.  
J. Biol. Chem. 263, 8232-8238, 1988  
A:Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regio  
A:Reference number: A28079; MUID:88228050; PMID:3372523  
A:Accession: A28079  
A:Molecule type: protein  
A:Residues: 834-842, 'X', 844-911 <KAW>  
A:Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate fo  
R:Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.  
Biochim. Biophys. Acta 998, 43-49, 1989  
A:Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3  
A:Reference number: S05523; MUID:90001294; PMID:2790053  
A:Accession: S05523  
A:Molecule type: protein  
A:Residues: 1-201; 220-292; 307-308, 'R', 310-312, 'S', 314-329, 'K', 331-333; 347-370 <YAN1>  
R:Cobb, C.E.; Beth, A.H.  
Biochemistry 29, 8283-8290, 1990  
A:Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyt  
A:Reference number: A35835; MUID:91070049; PMID:1701324  
A:Accession: A35835  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 361-364, 'X', 366-372; 424-429, 'X', 431-434 <COB>  
A:Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes  
R:Yannoukakos, D.; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.;  
Blood 78, 1117-1120, 1991  
A:Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the  
A:Reference number: A44933; MUID:91329825; PMID:1678289  
A:Accession: A44933  
A:Molecule type: protein  
A:Residues: 1-55, 'E', 57-69 <YAN2>  
A:Note: sequence extracted from NCBI backbone (NCBIP:49829)  
A:Note: sequence of a common polymorphic form designated band 3 Memphis

R:Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.  
J. Biol. Chem. 267, 19211-19217, 1992  
A:Title: A structural study of the membrane domain of band 3 by tryptic digestion. Co  
A:Reference number: A44116; MUID:92406862; PMID:1527044  
A:Accession: A44116  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 361-372; 390-399; 604-613; 632-639; 647-656; 699-729; 731-743; 761-781; 818-826 <  
A:Experimental source: erythrocyte  
A:Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:1138  
A:Note: a histidine residue essential for anion transport is suggested to be His-651,  
R:Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.  
J. Biol. Chem. 269, 1918-1926, 1994  
A:Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS  
A:Reference number: A49717; MUID:94124538; PMID:8294441  
A:Accession: A49717  
A:Molecule type: protein  
A:Residues: 427-436; 479-519; 538-540; 559-566; 809-817; 825-841; 849-857 <OKU>  
R:Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.  
J. Biochem. 122, 577-585, 1997  
A:Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fi  
A:Reference number: PC4403; MUID:98006310; PMID:9348087  
A:Accession: PC4403  
A:Molecule type: protein  
A:Residues: 361-911 <HAM>  
C:Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A d  
C:Comment: Band 3 has at least two functional domains. Its integral domain mediates a  
ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.  
C:Genetics:  
A:Gene: GDB:SLC4A1; EPB3  
A:Cross-references: GDB:119874; OMIM:109270  
A:Map position: 17q21-17q22  
C:Superfamily: band 3 anion transport protein  
C:Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; trans  
E:1-403/Region: cytoskeletal protein binding  
E:404-911/Region: anion antiporter  
F:405-427/Domain: transmembrane #status predicted <TM01>  
F:435-457/Domain: transmembrane #status predicted <TM02>  
F:459-479/Domain: transmembrane #status predicted <TM03>  
F:491-507/Domain: transmembrane #status predicted <TM04>  
F:522-542/Domain: transmembrane #status predicted <TM05>  
F:568-588/Domain: transmembrane #status predicted <TM06>  
F:604-624/Domain: transmembrane #status predicted <TM07>  
F:659-680/Domain: transmembrane #status predicted <TM08>  
F:701-721/Domain: transmembrane #status predicted <TM09>  
F:723-743/Domain: transmembrane #status predicted <TM10>  
F:764-780/Domain: transmembrane #status predicted <TM11>  
F:785-806/Domain: transmembrane #status predicted <TM12>  
F:839-859/Domain: transmembrane #status predicted <TM13>  
F:861-891/Domain: transmembrane #status predicted <TM14>  
F:1/Modified site: acetylated amino end (Met) #status experimental  
F:539,590,851/Binding site: anion (Lys) #status experimental  
F:642/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 104; DB 1; Length 911;  
Best Local Similarity 100.0%; Pred. No. 9e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GMPWLSATTVRSVTHANALT 20  
|||||  
Db 720 GMPWLSATTVRSVTHANALT 739  
|||||  
RESULT 3  
A25314  
band 3 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Aug-1999  
C:Accession: A25314; A26086; I49524; B25104  
R:Kopito, R.R.; Lodish, H.F.  
Nature 316, 234-238, 1985  
A:Title: Primary structure and transmembrane orientation of the murine anion exchange

A:Reference number: A25314; MUID:85268011; PMID:2410791  
A:Accession: A25314  
A:Molecule type: mRNA  
A:Residues: 1-929 <KOP>  
A:Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898  
R:Kopito, R.R.; Lodish, H.F.  
J. Cell. Biochem. 29, 1-17, 1985  
A:Title: Structure of the murine anion exchange protein.  
A:Reference number: A26086; MUID:86034211; PMID:3840489  
A:Accession: A26086  
A:Molecule type: mRNA  
A:Residues: 1-929 <K02>  
A:Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742  
R:Kopito, R.R.; Andersson, M.; Lodish, H.F.  
J. Biol. Chem. 262, 8035-8040, 1987  
A:Title: Structure and organization of the murine band 3 gene.  
A:Reference number: I49524; MUID:87250387; PMID:3036795  
A:Accession: I49524  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 4-707, 'X', 709-902 <RES>  
A:Cross-references: GB:X02756; NID:g192136; PIDN:AAA37278.1; PID:g553874  
R:Demuth, D.R.; Shove, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cloe, L.; Rovera  
EMBO J. 5, 1205-1214, 1986  
A:Title: Cloning and structural characterization of a human non-erythroid band 3-like pr  
A:Reference number: A91039; MUID:86274622; PMID:3015590  
A:Accession: B25104  
A:Molecule type: mRNA  
A:Residues: 11-466, 'S', 468-929 <DEM>  
A:Cross-references: GB:X03917; NID:g53042; PIDN:CAA27555.1; PID:g53043  
C:Genetics: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/  
A:Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/  
A:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein  
Query Match 100.0%; Score 104; DB 2; Length 929;  
Best Local Similarity 100.0%; Pred. No. 9.2e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GMPWLSATTVRSVTHANALT 20  
Db 738 GMPWLSATTVRSVTHANALT 757  
|||||  
RESULT 4  
I50159  
anion transporter - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 20-Aug-1999  
C:Accession: I50159  
R:Cox, J.V.; Lazarides, E.  
Mol. Cell. Biol. 8, 1327-1335, 1988  
A:Title: Alternative primary structures in the transmembrane domain of the chicken eryth  
A:Reference number: I50159; MUID:88216609; PMID:2835670  
A:Accession: I50159  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-844 <COX>  
A:Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212  
C:Superfamily: band 3 anion transport protein  
Query Match 96.2%; Score 100; DB 2; Length 844;  
Best Local Similarity 90.0%; Pred. No. 3.7e-08;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GMPWLSATTVRSVTHANALT 20  
Db 653 GMPWLSATTVRTITHANALT 672  
|||||  
RESULT 5  
A30816  
band 3 anion transport protein (clone pBIITC1) - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 16-Feb-1997  
C:Accession: A30816  
R:Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke,  
Mol. Cell. Biol. 8, 4416-4424, 1988  
A:Title: Two different mRNAs are transcribed from a single genomic locus encoding the  
A:Reference number: A30816; MUID:89039870; PMID:3185555  
A:Accession: A30816  
A:Molecule type: mRNA  
A:Residues: 1-922 <KIM>  
A:Cross-references: GB:M23404  
A:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein  
Query Match 96.2%; Score 100; DB 2; Length 922;  
Best Local Similarity 90.0%; Pred. No. 4.1e-08;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GMPWLSATTVRSVTHANALT 20  
Db 731 GMPWLSATTVRTITHANALT 750  
|||||  
RESULT 6  
S59861  
band 3 anion transport protein isoform b - rainbow trout  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Aug-1999  
C:Accession: S59861  
R:Fleivet, B.; Gabillat, N.; Borgese, F.; Motaïs, R.  
EMBO J. 14, 5158-5169, 1995  
A:Title: Expression of band 3 anion exchanger induces chloride current and taurine tr  
A:Reference number: S59861; MUID:96080151; PMID:7489705  
A:Accession: S59861  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-912 <FIE>  
A:Cross-references: EMBL:250848; NID:g1004316; PIDN:CAA90701.1; PID:g1004317  
C:Superfamily: band 3 anion transport protein  
Query Match 91.3%; Score 95; DB 2; Length 912;  
Best Local Similarity 90.0%; Pred. No. 2.7e-07;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GMPWLSATTVRSVTHANALT 20  
Db 727 GVPWLSAATVRSVTHANALT 746  
|||||  
RESULT 7  
S24318  
band 3 anion transport protein - rainbow trout  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Aug-1999  
C:Accession: S24318; S36083; S22173  
R:Huebner, S.; Michel, F.; Rudloff, V.; Appelhaus, H.  
Biochem. J. 285, 17-23, 1992  
A:Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derive  
A:Reference number: S24318; MUID:92344566; PMID:1637296  
A:Accession: S24318  
A:Molecule type: mRNA  
A:Residues: 1-918 <HUE1>  
A:Cross-references: EMBL:X61699  
A:Accession: S36083  
A:Molecule type: protein  
A:Residues: 71-89; 94-114; 570-588 <HUE2>  
R:Appelhaus, H.  
submitted to the EMBL Data Library, August 1991  
A:Reference number: S22173  
A:Accession: S22173  
A:Molecule type: mRNA  
A:Residues: 1-304, 'G', 306-918 <APP>  
A:Cross-references: EMBL:X61699; NID:g64308; PIDN:CAA43868.1; PID:g64309

C:Superfamily: band 3 anion transport protein  
C:Keywords: erythrocyte; transmembrane protein

Query Match 91.3%; Score 95; DB 2; Length 918;  
Best Local Similarity 90.0%; Pred. No. 2.7e-07;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
I:||||| ||||| ||||| |||||  
DB 733 GVPWLSAATVRSVTHANALT 752

#### RESULT 8

A:Residues: 1-865 <DEM>  
A:Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

Query Match 89.4%; Score 93; DB 2; Length 865;  
Best Local Similarity 85.0%; Pred. No. 5.3e-07;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
I:||||| ||||| ||||| |||||  
DB 674 GLPWLAATVRSVTHANALT 693

RESULT 9

band 3-related protein 2 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999  
C:Accession: A34911; A35770  
R:Kudrycki, K.E.; Newman, P.R.; Shull, G.E.  
J. Biol. Chem. 265, 462-471, 1990  
A:Title: cDNA cloning and tissue distribution of mRNAs for two proteins that are related  
A:Reference number: A34911; MUID:90094439; PMID:2294114  
A:Accession: A34911  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1234 <KUD>  
A:Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091  
R:Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990  
A:Title: Functional expression and subcellular localization of an anion exchanger cloned  
A:Reference number: A35770; MUID:90319095; PMID:2371270  
A:Accession: A35770  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-205, 'A', 207-924, 'PG', 927-1017, 'IV', 1020-1155, 'ID', 1158-1234 <LIN>  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

Query Match 89.4%; Score 93; DB 2; Length 1234;  
Best Local Similarity 85.0%; Pred. No. 7.8e-07;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
I:||||| ||||| ||||| |||||  
DB 1043 GLPWLAATVRSVTHANALT 1062

#### RESULT 10

A31789  
band 3-related protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 20-Aug-1999  
C:Accession: A31789  
R:Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.  
J. Biol. Chem. 263, 17092-17099, 1988  
A:Title: Cloning and characterization of a murine band 3-related cDNA from kidney and  
A:Reference number: A31789; MUID:89034212; PMID:3182834  
A:Accession: A31789  
A:Molecule type: mRNA  
A:Residues: 1-1237 <ALP>  
A:Cross-references: GB:J04036; NID:g192132; PIDN:AAA65505.1; PID:g309114  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

Query Match 89.4%; Score 93; DB 2; Length 1237;  
Best Local Similarity 85.0%; Pred. No. 7.8e-07;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
I:||||| ||||| ||||| |||||  
DB 1046 GLPWLAATVRSVTHANALT 1065

#### RESULT 11

A56764  
band 3-related protein, ileum - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 08-Sep-1995 #sequence\_revision 08-Sep-1995 #text\_change 20-Aug-1999  
C:Accession: A56764  
R:Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.  
Am. J. Physiol. 263, G345-G352, 1992  
A:Title: cDNA cloning and localization of a band 3-related protein from ileum.  
A:Reference number: A56764; MUID:93035730; PMID:1415547  
A:Accession: A56764  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1237 <CHO>  
A:Cross-references: GB:S45791; NID:g256659; PIDN:AAB23488.1; PID:g256660  
A:Experimental source: New Zealand White rabbit, ileal epithelial cells  
A:Note: sequence extracted from NCBI backbone (NCBIN:115180, NCBIP:115181)  
C:Superfamily: band 3 anion transport protein

Query Match 89.4%; Score 93; DB 2; Length 1237;  
Best Local Similarity 85.0%; Pred. No. 7.8e-07;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
I:||||| ||||| ||||| |||||  
DB 1046 GLPWLAATVRSVTHANALT 1065

#### RESULT 12

S21086  
anion exchange protein 2 - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1999  
C:Accession: S21086  
R:Gehrig, H.; Mueller, W.; Appelhans, H.  
Biochim. Biophys. Acta 1130, 326-328, 1992  
A:Title: Complete nucleotide sequence of band 3 related anion transport protein AE2 f  
A:Reference number: S21086; MUID:92223115; PMID:1562608  
A:Accession: S21086  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1240 <GEH>  
A:Cross-references: EMBL:X62137; NID:g28424; PIDN:CAA44067.1; PID:g28425  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

Query Match 89.4%; Score 93; DB 2; Length 1240;

Best Local Similarity 85.0%; Pred. No. 7.9e-07;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20  
I:|||||I|||||I|||||I  
DB 1049 GLPWLAATVRSVTHANALT 1068

RESULT 13  
A42497  
N:Alton exchanger 3, cardiac splice form - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 07-Dec-1999  
C:Accession: A42497; B42497  
R:Linn, S.C.; Kudrycki, K.E.; Shull, G.E.  
A:Title: The predicted translation product of a cardiac AE3 mRNA contains an N terminus  
gene, and identification of an alternative transcription initiation site.  
A:Reference number: A42497; MUID:92218461; PMID:1560021  
A:Accession: A42497  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1030 <LIN2>  
A:Cross-references: GB:M87060; NID:g202770  
A:Note: this translation is not annotated in GenBank entry RATAE3A, release 111.0; this  
A:Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)  
A:Accession: B42497  
A:Molecule type: DNA  
A:Residues: 1-73, 'E' <LIN2>  
A:Cross-references: GB:M87060; NID:g202770; PID:AAA40692.1; PID:g202771  
A:Experimental source: tissue type spleen  
C:Superfamily: band 3 anion transport protein  
C:Keywords: alternative splicing; cardiac muscle; heart; transmembrane protein

RESULT 14  
B34911  
band 3-related protein 3 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999  
C:Accession: B34911  
R:Kudrycki, K.E.; Newman, P.R.; Shull, G.E.  
J. Biol. Chem. 265, 462-471, 1990  
A:Title: cDNA cloning and tissue distribution of mRNAs for two proteins that are related  
A:Reference number: A34911; MUID:90094439; PMID:2294114  
A:Accession: B34911  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1227 <KUD>  
A:Cross-references: GB:J05167; NID:g203088; PIDN:AAA40798.1; PID:g203089  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

RESULT 15  
A33638

```

erythrocyte anion exchanger homolog AE3 - mouse
C:Species: Mus musculus (house mouse)
C:date: 02-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 20-Aug-1999
R:Accession: A33638
R:Kopito, R.R.; Lee, B.S.; Simmons, D.M.; Lindsey, A.E.; Morgans, C.W.; Schneider, K.
Cell 59, 927-937, 1989
A:title: Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion
A:Reference number: A3638; MUID:90075236; PMID:2686841
A:Accession: A33638
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1227 <KOP>
A:Cross-references: GB:M28383; NID:g191735; PIDN:AAA37184.1; PID:g309095
C:Superfamily: band 3 anion transport protein

Query Match      85.6%; Score 89; DB 2; Length 1227;
Best Local Similarity 80.0%; Pred. No. 3.5e-06;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1  GMPWLSATTVRSVTHANALT 20
      |:||||| ||||| |||||
Db      1037 GLFWLTAATVRSVTHVNALT 1056

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Job time : 18.25 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:41:03 ; Search time 17.25 Seconds  
(without alignments)  
111.500 Million cell updates/sec

Title: US-10-087-464-4  
Perfect score: 112  
Sequence: 1 DRILLFKPKYHPDVPYK 20  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	911	1 B3HU	band 3 anion trans
2	108	96.4	848	2 A33810	band 3 anion trans
3	108	96.4	929	2 A25314	band 3 protein - m
4	82	73.2	844	2 I30159	anion transporter
5	82	73.2	922	2 A30816	band 3 anion trans
6	74	66.1	865	2 A25104	band 3 protein, no
7	74	66.1	1234	2 A34911	band 3-related pro
8	74	66.1	1237	2 A31789	band 3-related pro
9	74	66.1	1237	2 A56764	band 3-related pro
10	74	66.1	1240	2 S21086	anion exchange pro
11	68	60.7	1030	2 A42497	anion exchanger 3,
12	68	60.7	1227	2 B34911	band 3-related pro
13	68	60.7	1227	2 A33638	erythrocyte anion
14	66	58.9	1119	2 T37460	probable sodium bi
15	66	58.9	1175	2 T22491	hypothetical prote
16	63	56.2	1035	2 T31336	sodium bicarbonate
17	62	55.4	1232	2 I38496	anion exchanger 3
18	50	44.6	468	1 B84540	acid phosphatase (
19	50	44.6	912	2 S59861	band 3 anion trans
20	50	44.6	918	2 S24318	band 3 anion trans
21	49	43.8	336	1 QBE40	BGLF2 protein - hu
22	49	43.8	469	1 H84669	acid phosphatase (
23	49	43.8	473	1 A59200	acid phosphatase (
24	49	43.8	1079	2 PC7034	Na+ bicarbonate co
25	48	42.9	334	2 B75095	probable histone d
26	48	42.9	335	1 H71071	hypothetical prote
27	48	42.9	413	2 T43810	methyaspatae am
28	48	42.9	605	2 C96940	sportulation specif
29	48	42.9	1035	2 T13962	sodium bicarbonate

RESULT 1

B3HU

Band 3 anion transport protein, erythrocyte - human  
N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha  
C:Species: Homo sapiens (man)  
C:Date: 03-Aug-1984 #sequence\_revision 03-Oct-1995 #text\_change 22-Jun-1999  
C:Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079;  
R:Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989  
A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange  
A:Reference number: A36218; MUID:90083213; PMID:2594752  
A:Accession: A36218  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-911 <LDX>  
A:Cross-references: GB:M27819; NID:gl78215; PIDN:AAA35514.1; PID:gl78216  
R:Tanner, M.J.A.; Martin, P.G.; High, S.  
Biochem. J. 256, 703-712, 1988  
A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra  
A:Reference number: S03074; MUID:89134172; PMID:3223947  
A:Accession: S03074  
A:Molecule type: mRNA  
A:Residues: 1-55,'E',57-911 <TAN>  
A:Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714  
R:Showe, L.C.; Ballantine, M.; Huebner, K.  
Genomics 1, 71-76, 1987  
A:Title: Localization of the gene for the erythroid anion exchange protein, band 3 (E  
A:Reference number: I39408; MUID:88031311; PMID:3478298  
A:Accession: I39408  
A:Molecule type: DNA  
A:Residues: 37-56 <SHO1>  
A:Cross-references: GB:M16978; NID:gl78217; PIDN:AAA51670.1; PID:gl78220  
A:Accession: I39409  
A:Molecule type: DNA  
A:Residues: 118-161 <SHO2>  
A:Cross-references: GB:M16979; NID:gl78218; PIDN:AAA51671.1; PID:g553169  
R:Drickamer, L.K.  
J. Biol. Chem. 253, 7242-7248, 1978  
A:Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Iden  
A:Reference number: A92237; MUID:79027186; PMID:701248  
A:Accession: A92237  
A:Molecule type: protein  
A:Residues: 1-3 <DRI>  
R:Mawby, W.J.; Findlay, J.B.C.  
Biochem. J. 205, 465-475, 1982  
A:Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-  
A:Reference number: A26507; MUID:83074521; PMID:7150226  
A:Accession: A26507  
A:Molecule type: protein  
A:Residues: 437-473;360-364,'D',366-369 <MAW>  
R:Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.  
J. Biol. Chem. 258, 7981-7990, 1983

ALIGNMENTS

30 48 42.9 1035 2 T14110 sodium bicarbonate  
31 48 42.9 1079 2 T14031 sodium bicarbonate  
32 47 42.0 234 2 F69019 conserved hypothet  
33 47 42.0 284 2 B84146 transglutaminase t  
34 47 42.0 466 1 T04599 acid phosphatase (  
35 47 42.0 466 1 F96603 acid phosphatase (  
36 46 41.1 137 2 T30143 hypothetical prote  
37 46 41.1 306 2 E72237 hypothetical prote  
38 46 41.1 468 2 G82329 replicative DNA he  
39 46 41.1 1156 2 T23748 hypothetical prote  
40 45 40.6 77 2 AH1642 hypothetical prote  
41 45 40.2 214 2 C42327 alpha 2,6-sialyltr  
42 45 40.2 403 2 A28451 beta-galactoside a  
43 45 40.2 406 2 A41734 beta-galactoside a  
44 45 40.2 431 1 A59201 acid phosphatase (  
45 45 40.2 434 2 S11967 nodule-specific hy

A:Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte  
 A:Reference number: A92430; MUID:83238395; PMID:6345535  
 A:Accession: A92430  
 A:Molecule type: protein  
 A:Residues: 1-10,'D',12-68,'E',69-200 <KAU>  
 R:Brook, C.J.; Tanner, M.J.A.; Kempf, C.  
 Biochem. J. 213, 577-586, 1993  
 A:Title: The human erythrocyte anion-transport protein.  
 A:Reference number: A90323; MUID:83308584; PMID:6615451  
 A:Accession: A90323  
 A:Molecule type: protein  
 A:Residues: 559-630 <BRO>  
 A:Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport  
 R:Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.  
 J. Biol. Chem. 263, 8232-8238, 1988  
 A:Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal region  
 A:Reference number: A28079; MUID:88228050; PMID:3372523  
 A:Accession: A28079  
 A:Molecule type: protein  
 A:Residues: 834-842,'X',844-911 <KAW>  
 A:Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate for  
 R:Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.  
 Biochim. Biophys. Acta 998, 43-49, 1989  
 A:Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3  
 A:Reference number: S05523; MUID:90001294; PMID:2790053  
 A:Accession: S05523  
 A:Molecule type: protein  
 A:Residues: 1-201;220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 <YAN1>  
 R:Cobb, C.E.; Beth, A.H.  
 Biochemistry 29, 8283-8290, 1990  
 A:Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyte  
 A:Reference number: A35835; MUID:91070049; PMID:1701324  
 A:Accession: A35835  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 361-364,'X',366-372;424-429,'X',431-434 <COB>  
 A:Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes  
 R:Yannoukakos, D.; Vasseur, C.; Briancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.  
 Blood 78, 1117-1120, 1991  
 A:Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the  
 A:Reference number: A44933; MUID:91329825; PMID:1678289  
 A:Accession: A44933  
 A:Molecule type: protein  
 A:Residues: 1-55,'E',57-69 <YAN2>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:49829)  
 R:Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.  
 J. Biol. Chem. 267, 19211-19217, 1992  
 A:Title: A structural study of the membrane domain of band 3 by tryptic digestion. Conf  
 A:Reference number: A44116; MUID:92406862; PMID:1527044  
 A:Accession: A44116  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <KAN>  
 A:Experimental source: erythrocyte  
 A:Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823,  
 R:Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.  
 J. Biol. Chem. 269, 1918-1926, 1994  
 A:Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4  
 A:Reference number: A49717; MUID:94124538; PMID:8294441  
 A:Accession: A49717  
 A:Molecule type: protein  
 A:Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>  
 A:Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport  
 R:Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.  
 J. Biochem. 122, 577-585, 1997  
 A:Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fide  
 A:Reference number: PC4403; MUID:98006310; PMID:9348087  
 A:Accession: PC4403  
 A:Molecule type: protein  
 A:Residues: 361-911 <HAM>  
 C:Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime

C:Comment: Band 3 has at least two functional domains. Its integral domain mediates a  
 ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.  
 C:Genetics:  
 A:Gene: GDB:SLC4A1; EPB3  
 A:Cross-references: GDB:119874; OMIM:109270  
 A:Map position: 17q21-17q22  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transmem  
 F:1-403/Region: cytoskeletal protein binding  
 F:404-911/Region: anion antiporter  
 F:405-427/Domain: transmembrane #status predicted <TM01>  
 F:435-437/Domain: transmembrane #status predicted <TM02>  
 F:459-479/Domain: transmembrane #status predicted <TM03>  
 F:491-507/Domain: transmembrane #status predicted <TM04>  
 F:522-542/Domain: transmembrane #status predicted <TM05>  
 F:568-588/Domain: transmembrane #status predicted <TM06>  
 F:604-624/Domain: transmembrane #status predicted <TM07>  
 F:659-680/Domain: transmembrane #status predicted <TM08>  
 F:701-721/Domain: transmembrane #status predicted <TM09>  
 F:723-743/Domain: transmembrane #status predicted <TM10>  
 F:764-780/Domain: transmembrane #status predicted <TM11>  
 F:785-806/Domain: transmembrane #status predicted <TM12>  
 F:839-859/Domain: transmembrane #status predicted <TM13>  
 F:861-881/Domain: transmembrane #status predicted <TM14>  
 F:1/Modified site: acetylated amino end (Met) #status experimental  
 F:539,590,851/Binding site: anion (Lys) #status experimental  
 F:642/Binding site: carboxylate (Asn) (covalent) #status predicted  
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 Best Local Similarity 100.08; Pred. No. 5.5e-09;  
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 QY 1 DRILLFKPKYHPDVPVK 20  
 DB 807 DRILLFKPKYHPDVPVK 826  
 RESULT 2  
 A33810  
 band 3 anion transport protein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Aug-1999  
 C:Accession: A33810  
 R:Kudrycki, K.E.; Shull, G.E.  
 J. Biol. Chem. 264, 8185-8192, 1989  
 A:Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr  
 A:Reference number: A33810; MUID:89255254; PMID:2722777  
 A:Accession: A33810  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-848 <KUD>  
 A:Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093  
 C:Superfamily: band 3 anion transport protein  
 C:Keywords: alternative splicing; transmembrane protein  
 Query Match 96.48; Score 108; DB 2; Length 848;  
 Best Local Similarity 95.08; Pred. No. 2.1e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRILLFKPKYHPDVPVK 20  
 DB 744 DRILLFKPKYHPDVPVK 763  
 RESULT 3  
 A25314  
 band 3 protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Aug-1999  
 C:Accession: A25314; A26086; I49524; B25104  
 R:Kopito, R.R.; Lodish, H.F.  
 Nature 316, 234-238, 1985  
 A:Title: Primary structure and transmembrane orientation of the murine anion exchange

C:Species: Gallus gallus (chicken)  
C:Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 16-Feb-1997  
C:Accession: A30816  
R:Kim, H.R.C.; Yew, N.S.; Ansoorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, M.; Mol. Cell. Biol. 8, 4416-4424, 1988  
A:Title: Two different mRNAs are transcribed from a single genomic locus encoding the A:Reference number: A30816; MUID:89039870; PMID:3185555  
A:Accession: A30816  
A:Molecule type: mRNA  
A:Residues: 1-922 <KIM>  
A:Cross-references: GB:M23404  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

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QY 1 DRILLFLPKPKYHPDVPYV 19  
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DB 818 DRILLLLMPKPKYHPKEPV 836

RESULT 6  
A25104  
band 3 protein, nonerythroid (MEB3) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C:Accession: A25104  
R:Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rov EMBO J. 5, 1205-1214, 1986  
A:Title: Cloning and structural characterization of a human non-erythroid band 3-like A:Reference number: A91039; MUID:86274622; PMID:3015590  
A:Accession: A25104  
A:Molecule type: mRNA  
A:Residues: 1-865 <DEM>  
A:Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

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Best Local Similarity 65.0%; Pred. No. 0.0034; 4; Indels 0; Gaps 0;  
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRILLFLPKPKYHPDVPYVK 20  
:|: || ||||| |||||  
DB 761 ERLHLLMLPKKHPDVTYVK 780

RESULT 7  
A34911  
band 3-related protein 2 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999  
C:Accession: A34911; A35770  
R:Kudrycki, K.E.; Newman, P.R.; Shull, G.E.  
J. Biol. Chem. 265, 462-471, 1990  
A:Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are rela A:Reference number: A34911; MUID:90094439; PMID:2294114  
A:Accession: A34911  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1234 <KUD>  
A:Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091  
R:Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R. Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990  
A:Title: Functional expression and subcellular localization of an anion exchanger clo A:Reference number: A35770; MUID:90319095; PMID:2371270  
A:Accession: A35770  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A:Molecule type: mRNA  
A:Residues: 1-205; A', 207-924; 'PG', 927-1017, 'IV', 1020-1155, 'ID', 1158-1234 <LIN>  
C:Superfamily: band 3 anion transport protein

RESULT 10  
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anion exchange protein 2 - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1999  
C;Accession: S21086  
R;Gehrig, H.; Mueller, W.; Appelhans, H.  
Biochim. Biophys. Acta 1130, 326-338, 1992

A:Accession: D54711  
A:Status: preliminary  
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A:Cross-references: GB:J05167; NID:9203088; PIDN:AAA40798.1; PID:g203089  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

R;Kershaw, J.  
submitted to the EMBL Data Library, June 1996  
A;Reference number: Z19570  
A;Accession: T22491  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-1175 <WILL>  
A;Cross-references: EMBL:Z75541; PIDN:CAA99853.1; GSPDB:GN00019; CESP:F52B5.1  
A;Experimental source: clone F52B5  
C;Genetics:  
A;Gene: CESP:F52B5.1  
A;Map position: 1  
A;Introns: 67/1; 190/3; 253/3; 636/1; 757/3; 1021/3; 1139/3  
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Best Local Similarity 60.0%; Pred. No. 0.079;  
Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0

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Db 921 DRLLLFNPMKYQPDYIYR 940

Search completed: September 3, 2003, 11:51:20

JOB TIME : 18.23 SECS

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:41:03 ; Search time 17.25 seconds  
(without alignments)  
111.500 Million cell updates/sec

Title: US-10-087-464-2

Perfect score: 98

Sequence: 1 SVTHANALTVNGKASTPGAA 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	911	1 B3HU	band 3 anion trans
2	91	92.9	848	2 A33810	band 3 anion trans
3	91	92.9	929	2 A25314	band 3 protein - m
4	73	74.5	865	2 A25104	band 3 protein, no
5	73	74.5	1234	2 A34911	band 3-related pro
6	73	74.5	1237	2 A31789	band 3-related pro
7	73	74.5	1237	2 A56764	band 3-related pro
8	73	74.5	1240	2 S21086	anion exchange pro
9	71	72.4	844	2 I50159	anion transporter
10	71	72.4	922	2 A30816	band 3 anion trans
11	63	64.3	912	2 S59861	band 3 anion trans
12	63	64.3	918	2 S24318	band 3 anion trans
13	61	62.2	1030	2 A24397	anion exchanger 3,
14	61	62.2	1227	2 B34911	band 3-related pro
15	61	62.2	1227	2 A33638	erythrocyte anion
16	61	62.2	1232	2 I38496	anion exchanger 3
17	57	58.2	357	2 S31828	band 3 anion trans
18	49	50.0	262	2 I64139	hypothetical prote
19	48	49.0	1655	2 E97835	hypothetical prote
20	47.5	48.5	409	2 H95911	probable ferredoxi
21	47	48.0	1300	2 S07575	outer membrane pro
22	45	45.9	1127	2 T28435	proline dehydrogen
23	44	44.9	407	2 T30585	transferrase homolo
24	42.5	43.4	707	2 A35804	nucleolin - human
25	42	42.9	303	2 B71638	cell division prot
26	42	42.9	343	2 E95911	probable transcrip
27	42	42.9	422	2 T09120	basic leucine zipp
28	42	42.9	1213	2 T19835	hypothetical prote
29	42	42.9	1616	2 T47801	hypothetical prote

## ALIGNMENTS

### RESULT 1

B3HU

Band 3 anion transport protein, erythrocyte - human

N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha  
C:Species: Homo sapiens (man)  
C:Date: 03-Aug-1984 #sequence\_revision 03-Oct-1995 #text change 22-Jun-1999  
C:Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079;  
R:Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989  
A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange  
A:Reference number: A36218; MUID:90083213; PMID:2594752  
A:Accession: A36218  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-911 <LUX>  
A:Cross-references: GB:M27819; NID:gl78215; PIDN:AAA35514.1; PID:gl78216  
R:Tanner, M.J.A.; Martin, P.G.; High, S.  
Biochem. J. 256, 703-712, 1988  
A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra  
A:Reference number: S03074; MUID:89134172; PMID:3223947  
A:Accession: S03074  
A:Molecule type: mRNA  
A:Residues: 1-55, 'E', 57-911 <TAN>  
A:Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714  
R:Shove, L.C.; Ballantine, M.; Huebner, K.  
Genomics 1, 71-76, 1987  
A:Title: Localization of the gene for the erythroid anion exchange protein, band 3 (E  
A:Reference number: I39408; MUID:88031311; PMID:3478298  
A:Accession: I39408  
A:Molecule type: DNA  
A:Residues: 37-56 <SHOI>  
A:Cross-references: GB:M16978; NID:gl78217; PIDN:AAA51670.1; PID:gl78220  
A:Accession: I39409  
A:Molecule type: DNA  
A:Residues: 118-161 <SHO2>  
A:Cross-references: GB:M16979; NID:gl78218; PIDN:AAA51671.1; PID:g553169  
R:Drickamer, L.K.  
J. Biol. Chem. 253, 7242-7248, 1978  
A:Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Iden  
A:Reference number: A92237; MUID:79027186; PMID:701248  
A:Accession: A92237  
A:Molecule type: protein  
A:Residues: 1-3 <DRI>  
R:Mawby, W.J.; Findlay, J.B.C.  
Biochem. J. 205, 465-475, 1982  
A:Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-  
A:Reference number: A26507; MUID:83074521; PMID:7150226  
A:Accession: A26507  
A:Molecule type: protein  
A:Residues: 437-473;360-364, 'D', 366-369 <MAW>  
R:Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.  
J. Biol. Chem. 258, 7981-7990, 1983

polyketide synthas  
hypothetical prote  
orf1 5' to fcc - S  
triosephosphate is  
triosephosphate is  
geranylgeranyl dip  
ABC transporter, s  
probable nucleic-bi  
probable RTX famil  
hypothetical prote  
latent transformin  
translation initia  
hypothetical prote  
hypothetical prote  
methionine.aminope

30 42 42.9 4613 2 T17409  
31 41.5 42.3 430 2 T12541  
32 41 41.8 122 2 A44238  
33 41 41.8 256 2 AH2775  
34 41 41.8 256 2 F97555  
35 41 41.8 329 2 C75400  
36 41 41.8 497 2 AG2724  
37 41 41.8 509 2 C97506  
38 41 41.8 603 2 H75272  
39 41 41.8 5188 2 B85547  
40 41 41.8 5291 2 F90696  
41 40.5 41.3 1820 2 A55494  
42 40 40.8 128 2 AE3544  
43 40 40.8 144 2 A82459  
44 40 40.8 206 2 T37094  
45 40 40.8 285 2 B87106

A;Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte  
A;Reference number: A92430; MUID:83238395; PMID:6345535  
A;Accession: A92430  
A;Molecule type: protein  
A;Residues: 1-10,'D',12-68,'E',69-200 <KAO>  
R;Brock, C.J.; Tanner, M.J.A.; Kempf, C.  
Biochem. J. 213, 577-586, 1983  
A;Title: The human erythrocyte anion-transport protein.  
A;Reference number: A90323; MUID:83308584; PMID:6615451  
A;Accession: A90323  
A;Molecule type: protein  
A;Residues: 559-630 <BRO>  
A;Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport  
R;Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.  
J. Biol. Chem. 263, 8232-8238, 1988  
A;Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal region  
A;Reference number: A28079; MUID:88228050; PMID:3372523  
A;Accession: A28079  
A;Molecule type: protein  
A;Residues: 834-842,'X',844-911 <KAW>  
A;Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate for  
R;Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.  
Biochim. Biophys. Acta 998, 43-49, 1989  
A;Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3  
A;Reference number: S05523; MUID:90001294; PMID:2790053  
A;Accession: S05523  
A;Molecule type: protein  
A;Residues: 1-201;220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 <YAN1>  
R;Cobb, C.E.; Beth, A.H.  
Biochemistry 29, 8283-8290, 1990  
A;Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyte  
A;Reference number: A35835; MUID:91070049; PMID:1701324  
A;Accession: A35835  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 361-364,'X',366-372;424-429,'X',431-434 <COB>  
A;Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes  
R;Yannoukakos, D.; Vasseur, C.; Briancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.;  
Blood 78, 1117-1120, 1991  
A;Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the  
A;Reference number: A44933; MUID:91329825; PMID:1678289  
A;Accession: A44933  
A;Molecule type: protein  
A;Residues: 1-55,'E',57-69 <YAN2>  
A;Note: sequence extracted from NCBI backbone (NCBIP:49829)  
R;Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.  
J. Biol. Chem. 267, 19211-19217, 1992  
A;Title: A structural study of the membrane domain of band 3 by tryptic digestion. Conf  
A;Reference number: A44116; MUID:92406862; PMID:1527044  
A;Accession: A44116  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <KAN>  
A;Experimental source: erythrocyte  
A;Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823,  
R;Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.  
J. Biol. Chem. 269, 1918-1926, 1994  
A;Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4  
A;Reference number: A49717; MUID:94124538; PMID:8294441  
A;Accession: A49717  
A;Molecule type: protein  
A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>  
A;Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport  
R;Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.  
J. Biochem. 122, 577-585, 1997  
A;Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel  
A;Reference number: PC4403; MUID:98006310; PMID:9348087  
A;Accession: PC4403  
A;Molecule type: protein  
A;Residues: 361-911 <HAM>  
C;Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime

C;Comment: Band 3 has at least two functional domains. Its integral domain mediates a  
ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.  
C;Genetics:  
A;Gene: GDB:SLC4A1; EPB3  
A;Cross-references: GDB:119874; OMIM:109270  
A;Map position: 17q21-17q22  
C;Superfamily: band 3 anion transport protein  
C;Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transmem  
F;1-403/Region: cytoskeletal protein binding  
F;404-911/Region: anion antiporter  
F;405-427/Domain: transmembrane #status predicted <TM01>  
F;435-457/Domain: transmembrane #status predicted <TM02>  
F;459-479/Domain: transmembrane #status predicted <TM03>  
F;491-507/Domain: transmembrane #status predicted <TM04>  
F;522-542/Domain: transmembrane #status predicted <TM05>  
F;568-588/Domain: transmembrane #status predicted <TM06>  
F;604-624/Domain: transmembrane #status predicted <TM07>  
F;659-680/Domain: transmembrane #status predicted <TM08>  
F;701-721/Domain: transmembrane #status predicted <TM09>  
F;723-743/Domain: transmembrane #status predicted <TM10>  
F;764-780/Domain: transmembrane #status predicted <TM11>  
F;785-806/Domain: transmembrane #status predicted <TM12>  
F;839-859/Domain: transmembrane #status predicted <TM13>  
F;861-881/Domain: transmembrane #status predicted <TM14>  
F;1/Modified site: acetylated amino end (Met) #status experimental  
F;539,590,851/Binding site: anion (Lys) #status experimental  
F;642/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 98; DB 1; Length 911;  
Best Local Similarity 100.0%; Pred. No. 5e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPGAA 20  
|||||  
Db 731 SVTHANALTVMGKASTPGAA 750

## RESULT 2

A33810  
band 3 anion transport protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Aug-1999  
C;Accession: A33810  
R;Kudrycki, K.E.; Shull, G.E.  
J. Biol. Chem. 264, 8185-8192, 1989  
A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr  
A;Reference number: A33810; MUID:89255254; PMID:2722777  
A;Accession: A33810  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-848 <KUD>  
A;Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093  
C;Superfamily: band 3 anion transport protein  
C;Keywords: alternative splicing; transmembrane protein

Query Match 92.9%; Score 91; DB 2; Length 848;  
Best Local Similarity 95.0%; Pred. No. 6.7e-07;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPGAA 20  
|||||  
Db 668 SVTHANALTVMGKASTPGAA 687

## RESULT 3

A25314  
band 3 protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Aug-1999  
C;Accession: A25314; A26086; I49524; B25104  
R;Kopito, R.R.; Lodish, H.F.  
Nature 316, 234-238, 1985  
A;Title: Primary structure and transmembrane orientation of the murine anion exchange



A:Reference number: A25314; MUID:85268011; PMID:2410791  
 A:Accession: A25314

A:Molecule type: mRNA

A:Residues: 1-929 <KOP>

A:Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898

R:Kopito, R.R.; Lodish, H.F., 1985

J. Cell. Biochem. 29, 1-17, 1985

A:Title: Structure of the murine anion exchange protein.

A:Reference number: A26086; MUID:86034211; PMID:3840489

A:Accession: A26086

A:Molecule type: mRNA

A:Residues: 1-929 <KOP>

A:Cross-references: GB:W29379; NID:g191741; PIDN:AAA37187.1; PID:g191742

R:Kopito, R.R.; Andersson, M.; Lodish, H.F.

J. Biol. Chem. 262, 8035-8040, 1987

A:Title: Structure and organization of the murine band 3 gene.

A:Reference number: I49524; MUID:87250387; PMID:3036795

A:Accession: I49524

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 4-707, 'X', 709-902 <RES>

A:Cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874

R:Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera

EMBO J. 5, 1205-1214, 1986

A:Title: Cloning and structural characterization of a human non-erythroid band 3-like pr

A:Reference number: A91039; MUID:86274622; PMID:3015590

A:Accession: B25104

A:Molecule type: mRNA

A:Residues: 11-466, 'S', 468-929 <DEM>

A:Cross-references: GB:X03917; NID:g53042; PIDN:CAA27555.1; PID:g53043

C:Genetics:

A:Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/

C:Superfamily: band 3 anion transport protein

C:Keywords: transmembrane protein

Query Match 92.9%; Score 91; DB 2; Length 929;

Best Local Similarity 95.0%; Pred. No. 7.4e-07;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPGAA 20

DB 749 SVTHANALTVMGKASPGAA 768

|||||

RESULT 4

A25104

band 3 protein, nonerythroid (MEB3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999

C:Accession: A25104

R:Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera

EMBO J. 5, 1205-1214, 1986

A:Title: Cloning and structural characterization of a human non-erythroid band 3-like pr

A:Reference number: A91039; MUID:86274622; PMID:3015590

A:Accession: A25104

A:Molecule type: mRNA

A:Residues: 1-865 <DEM>

A:Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121

C:Superfamily: band 3 anion transport protein

C:Keywords: transmembrane protein

Query Match 74.5%; Score 73; DB 2; Length 865;

Best Local Similarity 83.3%; Pred. No. 0.00068;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPG 18

DB 685 SVTHANALTVMSKAVAPG 702

|||||

RESULT 5

A34911

band 3-related protein 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999

C:Accession: A34911; A35770

R:Kudrycki, K.E.; Newman, P.R.; Shull, G.E.

J. Biol. Chem. 265, 462-471, 1990

A:Title: cDNA cloning and tissue distribution of mRNAs for two proteins that are rela

A:Reference number: A34911; MUID:90094439; PMID:2294114

A:Accession: A34911

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1234 <KUD>

A:Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091

R:Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.

Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990

A:Title: Functional expression and subcellular localization of an anion exchanger clo

A:Reference number: A35770; MUID:90319095; PMID:2371270

A:Accession: A35770

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA

A:Residues: 1-205, 'A', 207-924, 'PG', 927-1017, 'IV', 1020-1155, 'ID', 1158-1234 <LIN>

C:Superfamily: band 3 anion transport protein

C:Keywords: transmembrane protein

Query Match 74.5%; Score 73; DB 2; Length 1234;

Best Local Similarity 83.3%; Pred. No. 0.00099;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPG 18

DB 1054 SVTHANALTVMSKAVAPG 1071

|||||

RESULT 6

A31789

band 3-related protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 20-Aug-1999

C:Accession: A31789

R:Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.

J. Biol. Chem. 263, 17092-17099, 1988

A:Title: Cloning and characterization of a murine band 3-related cDNA from kidney and

A:Reference number: A31789; MUID:89034212; PMID:3182834

A:Accession: A31789

A:Molecule type: mRNA

A:Residues: 1-1237 <ALP>

A:Cross-references: GB:J04036; NID:g192132; PIDN:AAA65505.1; PID:g309114

C:Superfamily: band 3 anion transport protein

C:Keywords: transmembrane protein

Query Match 74.5%; Score 73; DB 2; Length 1237;

Best Local Similarity 83.3%; Pred. No. 0.00099;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPG 18

DB 1057 SVTHANALTVMSKAVAPG 1074

|||||

RESULT 7

A56764

band 3-related protein, ileum - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 08-Sep-1995 #sequence\_revision 08-Sep-1995 #text\_change 20-Aug-1999

C:Accession: A56764

R:Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.

Am. J. Physiol. 263, G345-G352, 1992

A:Title: cDNA cloning and localization of a band 3-related protein from ileum.

A:Reference number: A56764; MUID:93035730; PMID:1415547

A:Accession: A56764

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1237 <CHO>

A:Cross-references: GB:S45791; NID:g256659; PIDN:AAB23488.1; PID:g256660

A: Experimental source: New Zealand white rabbit, ileal epithelial cells  
 A: Note: sequence extracted from NCBI backbone (NCBIN:115180, NCBIPI:115181)  
 C: Superfamily: band 3 anion transport protein

Query Match 74.5%; Score 73; DB 2; Length 1237;  
 Best Local Similarity 83.3%; Pred. No. 0.00099;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPG 18  
 |||||  
 DB 1057 SVTHANALTVMSKAVAPG 1074

## RESULT 8

S21086  
 anion exchange protein 2 - human  
 C: Species: Homo sapiens (man)  
 C: Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1999  
 C: Accession: S21086  
 R: Gehrig, H.; Mueller, W.; Appelhans, H.  
 Biochim. Biophys. Acta 1130, 326-328, 1992  
 A: Title: Complete nucleotide sequence of band 3 related anion transport protein AE2 from  
 A: Reference number: S21086; MUID: 92223115; PMID: 1562608  
 C: Accession: S21086  
 A: Status: preliminary  
 A: Molecule type: mRNA  
 A: Residues: 1-1240 <GSH>  
 A: Cross-references: EMBL: X62137; NID: g28424; PIDN: CAA44067.1; PID: g28425  
 C: Superfamily: band 3 anion transport protein  
 C: Keywords: transmembrane protein

Query Match 74.5%; Score 73; DB 2; Length 1240;  
 Best Local Similarity 83.3%; Pred. No. 0.00099;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPG 18  
 |||||  
 DB 1060 SVTHANALTVMSKAVAPG 1077

## RESULT 9

I50159  
 anion transporter - chicken  
 C: Species: Gallus gallus (chicken)  
 C: Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 20-Aug-1999  
 C: Accession: I50159  
 R: Cox, J.V.; Lazarides, E.  
 Mol. Cell. Biol. 8, 1327-1335, 1988  
 A: Title: Alternative primary structures in the transmembrane domain of the chicken eryth  
 A: Reference number: I50159; MUID: 88216609; PMID: 2835670  
 C: Accession: I50159  
 A: Status: preliminary; translated from GB/EMBL/DBJ  
 A: Molecule type: mRNA  
 A: Residues: 1-844 <COX>  
 A: Cross-references: GB: M19496; NID: g211211; PIDN: AAA48604.1; PID: g211212  
 C: Superfamily: band 3 anion transport protein

Query Match 72.4%; Score 71; DB 2; Length 844;  
 Best Local Similarity 66.7%; Pred. No. 0.0014;  
 Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPG 18  
 :|||  
 DB 664 TITHANALTVVGSAPVG 681

## RESULT 10

A30816  
 band 3 anion transport protein (clone pBIIIC1) - chicken  
 C: Species: Gallus gallus (chicken)  
 C: Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 16-Feb-1997  
 C: Accession: A30816  
 R: Kim, H.R.C.; Yew, N.S.; Ansonge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, M.

Mol. Cell. Biol. 8, 4416-4424, 1988

A: Title: Two different mRNAs are transcribed from a single genomic locus encoding the  
 A: Reference number: A30816; MUID: 89039870; PMID: 3185555

A: Accession: A30816

A: Molecule type: mRNA

A: Residues: 1-922 <KIM>

A: Cross-references: GB: M23404

C: Superfamily: band 3 anion transport protein

C: Keywords: transmembrane protein

Query Match 72.4%; Score 71; DB 2; Length 922;  
 Best Local Similarity 66.7%; Pred. No. 0.0016;  
 Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTPG 18  
 :|||  
 DB 742 TITHANALTVVGSAPVG 759

## RESULT 11

S59861  
 band 3 anion transport protein isoform b - rainbow trout  
 C: Species: Oncorhynchus mykiss (rainbow trout)  
 C: Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 20-Aug-1999  
 C: Accession: S59861  
 R: Fievet, B.; Gabillat, N.; Borgese, F.; Motaïs, R.  
 EMBO J. 14, 5158-5169, 1995  
 A: Title: Expression of band 3 anion exchanger induces chloride current and taurine tr  
 A: Reference number: S59861; MUID: 96080151; PMID: 7489705  
 C: Accession: S59861  
 A: Status: preliminary; nucleic acid sequence not shown  
 A: Molecule type: mRNA  
 A: Residues: 1-912 <FIE>  
 A: Cross-references: EMBL: Z50848; NID: g1004316; PIDN: CAA90701.1; PID: g1004317  
 C: Superfamily: band 3 anion transport protein

Query Match 64.3%; Score 63; DB 2; Length 912;  
 Best Local Similarity 76.5%; Pred. No. 0.033;  
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTP 17  
 |||||  
 DB 738 SVTHANALTVMSKPKP 754

## RESULT 12

S24318  
 band 3 anion transport protein - rainbow trout  
 C: Species: Oncorhynchus mykiss (rainbow trout)  
 C: Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Aug-1999  
 C: Accession: S24318; S36083; S22173  
 R: Huebner, S.; Michel, F.; Rudloff, V.; Appelhans, H.  
 Biochem. J. 285, 17-23, 1992  
 A: Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derive  
 A: Reference number: S24318; MUID: 92344566; PMID: 1637296  
 C: Accession: S24318  
 A: Molecule type: mRNA  
 A: Residues: 1-918 <HUE1>  
 A: Cross-references: EMBL: X61699  
 A: Accession: S36083  
 A: Molecule type: protein  
 A: Residues: 71-89; 94-114; 570-588 <HUE2>  
 R: Appelhans, H.  
 submitted to the EMBL Data Library, August 1991  
 A: Reference number: S22173  
 C: Accession: S22173  
 A: Molecule type: mRNA  
 A: Residues: 1-304, G, 306-918 <APP>  
 A: Cross-references: EMBL: X61699; NID: 964308; PIDN: CAA43868.1; PID: g64309  
 C: Superfamily: band 3 anion transport protein  
 C: Keywords: erythrocyte; transmembrane protein

Query Match 64.3%; Score 63; DB 2; Length 918;

Best Local Similarity 76.5%; Pred. NO. 0.033;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTP 17  
DB 744 SVTHANALTMVGKPKP 760

## RESULT 13

A42497  
N:anion exchanger 3, cardiac splice form - rat  
N:Alternate names: AE3; chloride/bicarbonate exchanger 3  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 07-Dec-1999  
C:Accession: A42497; B42497  
R:Linn, S.C.; Kudrycki, K.E.; Shull, G.E.  
J. Biol. Chem. 267, 7927-7935, 1992  
A:Title: The predicted translation product of a cardiac AE3 mRNA contains an N terminus gene, and identification of an alternative transcription initiation site.  
A:Reference number: A42497; MUID:92218461; PMID:1560021  
A:Accession: A42497  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1030 <LIN1>  
A:Cross-references: GB:M87060; NID:g202770  
A:Note: This translation is not annotated in GenBank entry RATAE3A, release 111.0; this A:Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)  
A:Accession: B42497  
A:Molecule type: DNA  
A:Residues: 1-73, 'E' <LIN2>  
A:Cross-references: GB:M87060; NID:g202770; PIDN:AAA0692.1; PID:g202771  
A:Experimental source: tissue type spleen  
C:Superfamily: band 3 anion transport protein  
C:Keywords: alternative splicing; cardiac muscle; heart; transmembrane protein

Query Match 62.2%; Score 61; DB 2; Length 1030;

Best Local Similarity 72.2%; Pred. NO. 0.081;  
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPG 18  
DB 851 SVTHVNALTMVRTAIPG 868

## RESULT 14

B34911  
band 3-related protein 3 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999  
C:Accession: B34911  
R:Kudrycki, K.E.; Newman, P.R.; Shull, G.E.  
J. Biol. Chem. 265, 462-471, 1990  
A:Title: cDNA cloning and tissue distribution of mRNAs for two proteins that are related  
A:Reference number: B34911; MUID:90094439; PMID:2294114  
A:Accession: B34911  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1227 <KUD>  
A:Cross-references: GB:J05167; NID:g203088; PIDN:AAA40798.1; PID:g203089  
C:Superfamily: band 3 anion transport protein  
C:Keywords: transmembrane protein

Query Match 62.2%; Score 61; DB 2; Length 1227;

Best Local Similarity 72.2%; Pred. NO. 0.097;  
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPG 18  
DB 1048 SVTHVNALTMVRTAIPG 1065

## RESULT 15

A33638

erythrocyte anion exchanger homolog AE3 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Feb-1990 #sequence\_revision 02-Feb-1990 #text\_change 20-Aug-1999  
C:Accession: A33638  
R:Kopito, R.R.; Lee, B.S.; Simmons, D.M.; Lindsey, A.E.; Morgans, C.W.; Schneider, K.  
Cell 59, 927-937, 1989  
A:Title: Regulation of intracellular pH by a neuronal homolog of the erythrocyte anio  
A:Reference number: A33638; MUID:90075236; PMID:2686841

A:Accession: A33638  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1227 <KOP>  
A:Cross-references: GB:M28383; NID:g191735; PIDN:AAA37184.1; PID:g309095  
C:Superfamily: band 3 anion transport protein

Query Match 62.2%; Score 61; DB 2; Length 1227;

Best Local Similarity 72.2%; Pred. NO. 0.097;  
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPG 18  
DB 1048 SVTHVNALTMVRTAIPG 1065

Search completed: September 3, 2003, 11:51:18

Job time : 19.25 secs

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:41:03 ; Search time 17.25 Seconds  
(without alignments)  
111.500 Million cell updates/sec

Title: US-10-087-464-3  
Perfect score: 96  
Sequence: 1 GKASTFGAAAIQIEVKEQRI 20  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	911	1 B3HU	band 3 anion trans
2	89	92.7	848	2 A33810	band 3 anion trans
3	89	92.7	929	2 A25314	band 3 protein - m
4	61	63.5	844	2 I50159	anion transporter
5	61	63.5	922	2 A30816	band 3 anion trans
6	58	60.4	865	2 A25104	band 3 protein, no
7	58	60.4	1234	2 A34911	band 3-related pro
8	58	60.4	1237	2 A31789	band 3-related pro
9	58	60.4	1237	2 A56764	band 3-related pro
10	58	60.4	1240	2 S21086	anion exchange pro
11	54	56.2	357	2 S31828	band 3 anion trans
12	54	56.2	1030	2 A42497	anion exchanger 3,
13	54	56.2	1227	2 B34911	band 3-related pro
14	54	56.2	1227	2 A33638	erythrocyte anion
15	54	56.2	1232	2 I38496	anion exchanger 3
16	50	52.1	1317	2 T03748	apoptosis associat
17	48	50.0	346	2 F75377	ABC transporter, A
18	48	50.0	362	2 D82644	sugar-phosphate de
19	45	46.9	329	2 E82644	sugar-phosphate de
20	45	46.9	391	1 RKN2YA	polymenase-associa
21	45	46.9	391	1 RKN2ED	polymenase-associa
22	45	46.9	826	2 T28858	hypothetical prote
23	44	45.8	391	2 T36321	hypothetical prote
24	44	45.8	455	2 JC1224	nucleobindin precu
25	44	45.8	459	2 I55472	Calcium binding pr
26	44	45.8	1369	2 D86178	hypothetical prote
27	44	45.8	1495	2 T48429	hypothetical prote
28	43	44.8	324	2 F95386	protein [imported
29	43	44.8	416	2 D90938	probable transport

ALIGNMENTS

RESULT 1

B3HU  
band 3 anion transport protein, erythrocyte - human  
N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha  
C:Species: Homo sapiens (man)  
C:Date: 03-Aug-1984 #sequence-revision 03-Oct-1995 #text-change 22-Jun-1999  
C:Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079;  
R:Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.  
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989  
A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange  
A:Reference number: A36218; MUID:90083213; PMID:2594752  
A:Accession: A36218  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-911 <LDX>  
A:Cross-references: GB:M27819; NID:gl78215; PIDN:AAA35514.1; PID:gl78216  
R:Tanner, M.J.A.; Martin, P.G.; High, S.  
Biochem. J. 256, 703-712, 1988  
A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra  
A:Reference number: S03074; MUID:89134172; PMID:3223947  
A:Accession: S03074  
A:Molecule type: mRNA  
A:Residues: 1-55,'E',57-911 <TAN>  
A:Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714  
R:Shove, L.C.; Ballantine, M.; Huebner, K.  
Genomics 1, 71-76, 1987  
A:Title: Localization of the gene for the erythroid anion exchange protein, band 3 (E  
A:Reference number: I39408; MUID:88031311; PMID:3478298  
A:Accession: I39408  
A:Molecule type: DNA  
A:Residues: 37-56 <SHOL>  
A:Cross-references: GB:M16978; NID:gl78217; PIDN:AAA51670.1; PID:gl78220  
A:Accession: I39409  
A:Molecule type: DNA  
A:Residues: 118-161 <SHO>  
A:Cross-references: GB:M16979; NID:gl78218; PIDN:AAA51671.1; PID:g5553169  
R:Drickamer, L.K.  
J. Biol. Chem. 253, 7242-7248, 1978  
A:Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Iden  
A:Reference number: A92237; MUID:79027186; PMID:701248  
A:Accession: A92237  
A:Molecule type: protein  
A:Residues: 1-3 <DRI>  
R:Mawdy, W.J.; Findlay, J.B.C.  
Biochem. J. 205, 465-475, 1982  
A:Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-  
A:Reference number: A26507; MUID:83074521; PMID:7150226  
A:Accession: A26507  
A:Molecule type: protein  
A:Residues: 437-473;360-364,'D',366-369 <MAW>  
R:Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.  
J. Biol. Chem. 258, 7981-7990, 1983

probable transport  
hypothetical metab  
coronin-like prote  
non-histone chromo  
D-alanyl-D-alanine  
hypothetical prote  
probable myosin he  
probable sodium bi  
hypothetical prote  
collagen - nematod  
acidic calmodulin-  
flagellar biosynth  
flagellar biosynth  
probable dimethyla  
protein F5M15.22 [

A;Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte  
 A;Reference number: A92430; MUID:83238395; PMID:6345535  
 A;Accession: A92430  
 A;Molecule type: protein  
 A;Residues: 1-10,'D',12-68,'E',69-200 <KAD>  
 R;Brock, C.J.; Tanner, M.J.A.; Kempf, C.  
 Biochem. J. 213, 577-586, 1983  
 A;Title: The human erythrocyte anion-transport protein.  
 A;Reference number: A90323; MUID:83308584; PMID:6615451  
 A;Accession: A90323  
 A;Molecule type: protein  
 A;Residues: 559-630 <BR>  
 A;Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport  
 R;Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.  
 J. Biol. Chem. 263, 8232-8238, 1988  
 A;Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal region  
 A;Reference number: A28079; MUID:88228050; PMID:3372523  
 A;Accession: A28079  
 A;Molecule type: protein  
 A;Residues: 834-842,'X',844-911 <KAW>  
 A;Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate for  
 R;Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.  
 Biochim. Biophys. Acta 998, 43-49, 1989  
 A;Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3  
 A;Reference number: S05523; MUID:90001294; PMID:2790053  
 A;Accession: S05523  
 A;Molecule type: protein  
 A;Residues: 1-201;220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 <YAN1>  
 R;Cobb, C.E.; Beth, A.H.  
 Biochemistry 29, 8283-8290, 1990  
 A;Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyte  
 A;Reference number: A35835; MUID:91070049; PMID:1701324  
 A;Accession: A35835  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 361-364,'X',366-372;424-429,'X',431-434 <COB>  
 A;Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes  
 R;Yannoukakos, D.; Vasseur, C.; Briancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.;  
 Blood 78, 1117-1120, 1991  
 A;Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the  
 A;Reference number: A44933; MUID:91329825; PMID:1678289  
 A;Accession: A44933  
 A;Molecule type: protein  
 A;Residues: 1-55,'E',57-69 <YAN2>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:49829)  
 R;Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.  
 J. Biol. Chem. 267, 19211-19217, 1992  
 A;Title: A structural study of the membrane domain of band 3 by tryptic digestion. Conf  
 A;Reference number: A44116; MUID:92406862; PMID:1527044  
 A;Accession: A44116  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <KAN>  
 A;Experimental source: erythrocyte  
 A;Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823,  
 R;Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.  
 J. Biol. Chem. 269, 1918-1926, 1994  
 A;Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4  
 A;Reference number: A49717; MUID:94124538; PMID:8294441  
 A;Accession: A49717  
 A;Molecule type: protein  
 A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>  
 A;Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport  
 R;Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.  
 J. Biochem. 122, 577-585, 1997  
 A;Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fide  
 A;Reference number: PC4403; MUID:98006310; PMID:9348087  
 A;Accession: PC4403  
 A;Molecule type: protein  
 A;Residues: 361-911 <HAM>  
 C;Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dimer

C;Comment: Band 3 has at least two functional domains. Its integral domain mediates a  
 cing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.  
 C;Genetics:  
 A;Gene: GDB:SLC4A1; EPB3  
 A;Cross-references: GDB:119874; OMIM:109270  
 A;Map position: 17q21-17q22  
 C;Superfamily: band 3 anion transport protein  
 C;Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transmembrane  
 F;1-403/Region: cytoskeletal protein binding  
 F;404-911/Region: anion transporter  
 F;405-427/Domain: transmembrane status predicted <TM01>  
 F;435-457/Domain: transmembrane status predicted <TM02>  
 F;459-479/Domain: transmembrane status predicted <TM03>  
 F;491-507/Domain: transmembrane status predicted <TM04>  
 F;522-542/Domain: transmembrane status predicted <TM05>  
 F;568-588/Domain: transmembrane status predicted <TM06>  
 F;604-624/Domain: transmembrane status predicted <TM07>  
 F;659-680/Domain: transmembrane status predicted <TM08>  
 F;701-721/Domain: transmembrane status predicted <TM09>  
 F;723-743/Domain: transmembrane status predicted <TM10>  
 F;764-780/Domain: transmembrane status predicted <TM11>  
 F;785-806/Domain: transmembrane status predicted <TM12>  
 F;839-859/Domain: transmembrane status predicted <TM13>  
 F;861-881/Domain: transmembrane status predicted <TM14>  
 F;Modified site: acetylated amino end (Met) #status experimental  
 F;539-590.851/Binding site: anion (Lys) #status experimental  
 F;642/Binding site: carboxylate (Asn) (covalent) #status predicted  
 Query Match 100.0%; Score 96; DB 1; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GKASTPGAAAIQIEVKEQRI 20  
 Db 742 GKASTPGAAAIQIEVKEQRI 761  
 RESULT 2  
 A33810  
 band 3 anion transport protein - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Aug-1999  
 C;Accession: A33810  
 R;Kudrycki, K.E.; Shull, G.E.  
 J. Biol. Chem. 264, 8185-8192, 1989  
 A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr  
 A;Reference number: A33810; MUID:89255254; PMID:2722777  
 A;Accession: A33810  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-848 <KUD>  
 A;Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093  
 C;Superfamily: band 3 anion transport protein  
 C;Keywords: alternative splicing; transmembrane protein  
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 Best Local Similarity 95.0%; Pred. No. 1.2e-05;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GKASTPGAAAIQIEVKEQRI 20  
 Db 679 GKASTPGAAAIQIEVKEQRI 698  
 RESULT 3  
 A25314  
 band 3 protein - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 22-Jul-1987 #sequence\_revision 22-Jul-1987 #text\_change 20-Aug-1999  
 C;Accession: A25314; A26086; I49524; B25104  
 R;Kopito, R.R.; Lodish, H.F.  
 Nature 316, 234-238, 1985  
 A;Title: Primary structure and transmembrane orientation of the murine anion exchange

C;Species: Gallus gallus (chicken)  
C;Date: 01-Dec-1989 #sequence\_revision 30-Sep-1991 #text\_change 16-Feb-1997  
C;Accession: A30816  
R;Klm, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, M.; Mol. Cell. Biol. 8, 4416-4424, 1988  
A;Title: Two different mRNAs are transcribed from a single genomic locus encoding the A;Reference number: A30816; MUID:89039870; PMID:3185555  
A;Accession: A30816  
A;Molecule type: mRNA  
A;Residues: 1-922 <KIM>  
A;Cross-references: GB:M23404  
C;Superfamily: band 3 anion transport protein  
C;Keywords: transmembrane protein

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Best Local Similarity 60.0%; Pred. No. 0.27;  
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GKASTPGAAAIQIEVKEQRI 20  
||||| || || |||||:  
Db 753 GKSAVPGERAHIVEVKEQRL 772

RESULT 6  
A25104  
band 3 protein, nonerythroid (WEB3) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Aug-1999  
C;Accession: A25104  
R;Demuth, D.R.; Shove, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Roy EMBO J. 5, 1205-1214, 1986  
A;Title: Cloning and structural characterization of a human non-erythroid band 3-like A;Reference number: A91039; MUID:86274622; PMID:3015590  
A;Accession: A25104  
A;Molecule type: mRNA  
A;Residues: 1-865 <DEM>  
A;Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121  
C;Superfamily: band 3 anion transport protein  
C;Keywords: transmembrane protein

Query Match 60.4%; Score 58; DB 2; Length 865;  
Best Local Similarity 63.2%; Pred. No. 0.73;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KASTPGAAAIQIEVKEQRI 20  
|| || :|||||:  
Db 697 KAVAPGDKPKIEVKEQRV 715

RESULT 7  
A34911  
band 3-related protein 2 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 20-Aug-1999  
C;Accession: A34911; A35770  
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.  
J. Biol. Chem. 265, 462-471, 1990  
A;Title: cDNA cloning and tissue distribution of mRNAs for two proteins that are rela A;Reference number: A34911; MUID:90094439; PMID:2294114  
A;Accession: A34911

A:status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1234 <KUD>  
A:Cross-references: GB:J05166; NID:q203090; PID:AAA40799.1; PID:q203091

R.; Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, K.; Lee, B.S.; Koplo, R.K. Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990

A: Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
A: Molecule type: mRNA  
A: Residues: 1-205, 'A', 'PG', '927-1017', 'IV', 1020-1155, 'ID', 1158-1234 <LIN>  
C: Superfamily: band 3 anion transport protein

C;Keywords: transmembrane protein

Query Match 60.4%; Score 58; DB 2; Length 1234;  
Best Local Similarity 63.2%; Pred. No. 1;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 2 KASTPGAAQIOEVKEQRI 20  
|| || :|||||  
Db 1066 KAVAPGDKPKIQEVKEQRV 1084

## RESULT 8

A31789  
band 3-related protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 20-Aug-1999  
C;Accession: A31789  
R;Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.  
J. Biol. Chem. 263, 17092-17099, 1988  
A;Title: Cloning and characterization of a murine band 3-related cDNA from kidney and fr  
A;Accession number: A31789; UID:89034212; PMID:3182834  
A;Accession: A31789  
A;Molecule type: mRNA  
A;Residues: 1-1237 <ALP>  
A;Cross-references: GB:J04036; NID:g192132; PIDN:AAA65505.1; PID:g309114  
C;Superfamily: band 3 anion transport protein  
C;Keywords: transmembrane protein

Query Match 60.4%; Score 58; DB 2; Length 1237;  
Best Local Similarity 63.2%; Pred. No. 1;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 2 KASTPGAAQIOEVKEQRI 20  
|| || :|||||  
Db 1069 KAVAPGDKPKIQEVKEQRV 1087

## RESULT 9

A56764  
band 3-related protein, ileum - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 08-Sep-1995 #sequence\_revision 08-Sep-1995 #text\_change 20-Aug-1999  
C;Accession: A56764  
R;Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.  
Am. J. Physiol. 263, G345-G352, 1992  
A;Title: cDNA cloning and localization of a band 3-related protein from ileum.  
A;Reference number: A56764; UID:93035730; PMID:1415547  
A;Accession: A56764  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1237 <CHO>  
A;Cross-references: GB:S45791; NID:g256659; PIDN:AAB23488.1; PID:g256660  
A;Experimental source: New Zealand White rabbit, ileal epithelial cells  
A;Note: sequence extracted from NCBI backbone (NCBIN:115180, NCBI:P:115181)  
C;Superfamily: band 3 anion transport protein

Query Match 60.4%; Score 58; DB 2; Length 1237;  
Best Local Similarity 63.2%; Pred. No. 1;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 2 KASTPGAAQIOEVKEQRI 20  
|| || :|||||  
Db 1069 KAVAPGDKPKIQEVKEQRV 1087

## RESULT 10

S21086  
anion exchange protein 2 - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1999  
C;Accession: S21086  
R;Gehrig, H.; Mueller, W.; Appelhaus, H.  
Biochim. Biophys. Acta 1130, 326-328, 1992

A;Title: Complete nucleotide sequence of band 3 related anion transport protein AE2 f  
A;Reference number: S21086; UID:92223115; PMID:1562608  
A;Accession: S21086  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1240 <GEH>  
A;Cross-references: EMBL:X62137; NID:g28424; PIDN:CAA44067.1; PID:g28425  
C;Superfamily: band 3 anion transport protein  
C;Keywords: transmembrane protein

Query Match 60.4%; Score 58; DB 2; Length 1240;  
Best Local Similarity 63.2%; Pred. No. 1;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KASTPGAAQIOEVKEQRI 20  
|| || :|||||  
Db 1072 KAVAPGDKPKIQEVKEQRV 1090

## RESULT 11

S31828  
band 3 anion transport protein - human (fragment)  
N;Alternate names: anion exchange protein 3  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Aug-1999  
C;Accession: S31828  
R;Gehrig, H.; Appelhaus, H.  
submitted to the EMBL Data Library, January 1993  
A;Reference number: S31828  
A;Accession: S31828  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-357 <GEH>  
A;Cross-references: EMBL:X70797; NID:g28427; PIDN:CAA50067.1; PID:g939883  
C;Superfamily: band 3 anion transport protein

Query Match 56.2%; Score 54; DB 2; Length 357;  
Best Local Similarity 61.1%; Pred. No. 1.3;  
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ASTPGAAQIOEVKEQRI 20  
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Db 283 AIAPGDKPKIQEVKEQRV 300

## RESULT 12

A42497  
anion exchanger 3, cardiac splice form - rat  
N;Alternate names: AE3; chloride/bicarbonate exchanger 3  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 07-Dec-1999  
C;Accession: A42497; B42497  
R;Linn, S.C.; Kudrycki, K.E.; Shull, G.E.  
J. Biol. Chem. 267, 7927-7935, 1992  
A;Title: The predicted translation product of a cardiac AE3 mRNA contains an N termin  
gene, and identification of an alternative transcription initiation site.  
A;Reference number: A42497; UID:92218461; PMID:1560021  
A;Accession: A42497  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-1030 <LIN1>  
A;Cross-references: GB:M87060; NID:g202770  
A;Note: This translation is not annotated in GenBank entry RATAE3A, release 111.0; th  
A;Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBI:P:96975)  
A;Accession: B42497  
A;Molecule type: DNA  
A;Residues: 1-73, 'E', <LIN2>  
A;Cross-references: GB:M87060; NID:g202770; PIDN:AAA40692.1; PID:g202771  
A;Experimental source: tissue type spleen  
C;Superfamily: band 3 anion transport protein  
C;Keywords: alternative splicing; cardiac muscle; heart; transmembrane protein

Query Match 56.2%; Score 54; DB 2; Length 1030;



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RESULT 15
I38496
anion exchanger 3 brain isoform - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 20-Aug-1999
C:Accession: I38496
R:Yannoukakos, D.; Stuart-Willey, A.; Fernandez, H.; Fey, P.; Duyk, G.; Alper, S.
Circ. Res. 75, 603-614, 1994
A:Title: Molecular cloning, expression, and chromosomal localization of two isoforms of
A:Reference number: I38496; MUID:95098042; PMID:7923606
A:Accession: I38496
A>Status: preliminary; translated from GB/EMBL/DBRJ

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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:40:18 ; Search time 44.5 Seconds  
(without alignments)  
115.979 Million cell updates/sec

Title: US-10-087-464-3  
Perfect score: 96  
Sequence: 1 GKASTPGAAQIQEVKEQRI 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:.\*  
1: sp\_archaea:.\*  
2: sp\_bacteria:.\*  
3: sp\_fungi:.\*  
4: sp\_human:.\*  
5: sp\_invertebrate:.\*  
6: sp\_mammal:.\*  
7: sp\_mhc:.\*  
8: sp\_organelle:.\*  
9: sp\_phase:.\*  
10: sp\_plant:.\*  
11: sp\_rdent:.\*  
12: sp\_virus:.\*  
13: sp\_vertebrate:.\*  
14: sp\_unclassified:.\*  
15: sp\_rvirus:.\*  
16: sp\_bacteriap:.\*  
17: sp\_archaeap:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	92.7	849	11 Q91ZE7	Q91ZE7 rattus norv
2	70	72.9	855	6 Q9TUQ0	Q9TUQ0 bos taurus
3	70	72.9	930	6 Q9XSW5	Q9XSW5 bos taurus
4	61	63.5	844	13 Q90579	Q90579 gallus gall
5	58	60.4	103	11 Q35225	Q35225 cynomys lud
6	58	60.4	466	11 Q99LT5	Q99LT5 mus musculu
7	58	60.4	622	6 Q9TU75	Q9TU75 sus scrofa
8	58	60.4	1159	4 Q9TAG3	Q9TAG3 homo sapien
9	58	60.4	1219	13 Q90710	Q90710 gallus gall
10	58	60.4	1227	4 Q9UEX4	Q9UEX4 homo sapien
11	58	60.4	1232	4 Q9UEX5	Q9UEX5 homo sapien
12	58	60.4	1241	4 Q99654	Q99654 homo sapien
13	58	60.4	1241	4 Q99656	Q99656 homo sapien
14	54	56.2	357	4 Q99416	Q99416 homo sapien
15	54	56.2	357	4 Q13717	Q13717 homo sapien
16	54	56.2	1030	11 Q9ERP4	Q9ERP4 mus musculu

17	54	56.2	1227	11	Q9ERP5
18	50	52.1	160	13	P79877
19	50	52.1	993	11	Q8CHE2
20	50	52.1	1317	11	Q35211
21	50	52.1	1317	11	Q8CB63
22	48	50.0	346	16	Q9RU15
23	48	50.0	362	16	Q9PC05
24	47	49.0	394	16	Q986H6
25	45	46.9	329	16	Q9PC04
26	45	46.9	391	12	Q8QV71
27	45	46.9	391	12	Q9DQA3
28	45	46.9	391	12	Q910S3
29	45	46.9	391	12	Q9J4L6
30	45	46.9	391	12	Q8QY72
31	45	46.9	729	13	Q8AVI6
32	45	46.9	881	5	Q21664
33	45	46.9	1253	5	Q8MSP0
34	45	46.9	1253	5	Q9VPP2
35	45	46.9	1837	5	Q9VCZ9
36	44	45.8	391	16	Q9X8H5
37	44	45.8	459	11	Q8BRD3
38	44	45.8	467	5	Q95SW2
39	44	45.8	475	16	Q8FGX7
40	44	45.8	512	6	Q95KP5
41	44	45.8	716	11	Q8BN92
42	44	45.8	914	5	Q8MRK3
43	44	45.8	1036	6	Q8MKF0
44	44	45.8	1157	10	Q8H6X1
45	44	45.8	1161	5	Q8IQD4

#### ALIGNMENTS

#### RESULT 1

Q91ZE7 ID Q91ZE7 PRELIMINARY; PRT; 849 AA.  
AC Q91ZE7;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Band 3 anion exchange protein.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Colon;  
RA Ye H., Binder H.J., Rajendran V.M.;  
RT "Molecular cloning and characterization of band 3 anion exchange protein (AEL) mRNA from rat colon."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY030082; AAK38733.1;  
DR InterPro; IPR001717; Anion\_exchange.  
DR InterPro; IPR003020; HCO3\_cotransp.  
DR Pfam; PF00955; HCO3\_cotransp; 1.  
DR PRINTS; PR01231; HCO3TRNSPORT.  
DR TIGRFAMs; TIGR00834; ae; 1.  
DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
SQ SEQUENCE 849 AA; 94312 MW; E4B200780CB07D3A CRC64;

Query Match 92.7%; Score 89; DB 11; Length 849;  
Best Local Similarity 95.0%; Pred. No. 9.7e-06;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKASTPGAAQIQEVKEQRI 20

Db 680 GKASGPGAAQIQEVKEQRI 699

#### RESULT 2



DR Pfam: PF00955; HCO3\_cotransp; 1.  
 FT NON\_TER 1  
 RC TISSUE=Stomach;  
 RX MEDLINE=99315230; PubMed=10387099;  
 SQ SEQUENCE 103 AA; 11012 MW; 29A99247E768B455 CRC64;

Query Match 60.4%; Score 58; DB 11; Length 103;  
 Best Local Similarity 63.2%; Pred. No. 0.11;  
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KASTPGAAAQIQEVKEQRI 20  
 II II :|||||  
 Db 67 KAVAPGDKPKIQEVKEQRV 85

## RESULT 6

Q99LT5 PRELIMINARY; PRT; 466 AA.

AC Q99LT5: 01-JUN-2001 (TremBLrel. 17, Created)  
 DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
 DE Hypothetical 52.0 kDa protein (Fragment).  
 GN SLCA42.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC002234; AAH02234.1; -  
 DR MGI:109351; SLCA42.  
 DR InterPro: IPR001717; Anion\_exchange.  
 DR InterPro: IPR003020; HCO3\_cotransp.  
 DR Pfam: PF00955; HCO3\_cotransp; 1.  
 DR PRINTS: PR01231; HCO3TRNSPORT.  
 DR TIGRFAMs: TIGR00834; ae; 1.  
 DR PROSITE: PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 466 AA; 52003 MW; 481C1108E28D03B1 CRC64;

Query Match 60.4%; Score 58; DB 11; Length 466;  
 Best Local Similarity 63.2%; Pred. No. 0.57;  
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KASTPGAAAQIQEVKEQRI 20  
 II II :|||||  
 Db 298 KAVAPGDKPKIQEVKEQRV 316

## RESULT 7

Q99LT5 PRELIMINARY; PRT; 622 AA.

AC Q99LT5: 01-MAY-2000 (TremBLrel. 13, Created)  
 DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
 DE Chloride-bicarbonate anion exchanger AE2 (Fragment).  
 GN AE2.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Stomach;  
 RX MEDLINE=96339307; PubMed=8756692;  
 RA Zolotarev A.S.; Chernova M.N.; Yannoukatos D.; Alper S.L.;  
 RT "Proteolytic cleavage sites of native AE2 anion exchanger in gastric  
 mucosal membranes.";  
 RL Biochemistry 35:10367-10376(1996).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Stomach;  
 RX MEDLINE=99315230; PubMed=10387099;  
 RA Zolotarev A.S.; Shmukler B.E.; Alper S.L.;  
 RT "AE2 anion exchanger polypeptide is a homooligomer in pig gastric  
 membranes: a chemical cross-linking study.";  
 RL Biochemistry 38:8521-8531(1999).  
 DR EMBL: AF120099; AAF00977.1; -  
 DR HSP: P02730; 1BTO.  
 DR InterPro: IPR001717; Anion\_exchange.  
 DR InterPro: IPR003020; HCO3\_cotransp.  
 DR Pfam: PF00955; HCO3\_cotransp; 1.  
 DR PRINTS: PR01231; HCO3TRNSPORT.  
 DR TIGRFAMs: TIGR00834; ae; 1.  
 DR PROSITE: PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE: PS00220; ANION\_EXCHANGER\_2; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 622 AA; 68713 MW; 58B013462C36E1DC CRC64;

Query Match 60.4%; Score 58; DB 6; Length 622;  
 Best Local Similarity 63.2%; Pred. No. 0.77;  
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KASTPGAAAQIQEVKEQRI 20  
 II II :|||||  
 Db 454 KAVAPGDKPKIQEVKEQRV 472

## RESULT 8

Q8TAG3 PRELIMINARY; PRT; 1159 AA.

AC Q8TAG3: 01-JUN-2002 (TremBLrel. 21, Created)  
 DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
 DE Similar to solute carrier family 4, anion exchanger, member 2  
 DE (Erythrocyte membrane protein band 3-like 1).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC028601; AAH28601.1; -  
 DR InterPro: IPR001717; Anion\_exchange.  
 DR InterPro: IPR003020; HCO3\_cotransp.  
 DR Pfam: PF00955; HCO3\_cotransp; 1.  
 DR TIGRFAMs: TIGR00834; ae; 1.  
 DR PROSITE: PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE: PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1159 AA; 127747 MW; 9F083A2BE8FF5D74 CRC64;

Query Match 60.4%; Score 58; DB 4; Length 1159;  
 Best Local Similarity 63.2%; Pred. No. 1.5;  
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KASTPGAAAQIQEVKEQRI 20  
 II II :|||||  
 Db 991 KAVAPGDKPKIQEVKEQRV 1009

## RESULT 9

Q90710 PRELIMINARY; PRT; 1219 AA.

AC Q90710: 01-NOV-1996 (TremBLrel. 01, Created)  
 DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
 DE AE2-1 anion exchanger.

GN AE2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 ON NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Proventriculus;  
 RX MEDLINE=96224107; PubMed=8621532;  
 RA Cox K.H., Adair-Kirk T.L., Cox J.V.;  
 RT "Variant AE2 anion exchanger transcripts accumulate in multiple cell  
 RL types in the chicken gastric epithelium.";  
 DR J. Biol. Chem. 271:8895-8902(1996).  
 DR EMBL; U48889; AAC59881.1; -;  
 DR HSSP; P02730; 1BTO.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1219 AA; 135288 MW; 25F42A73C3483B21 CRC64;  
  
 Query Match 60.4%; Score 58; DB 13; Length 1219;  
 Best Local Similarity 63.2%; Pred. No. 1.6;  
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
 QY 2 KASTPGAAAOIQEVKEORI 20  
 DB 1052 KAVAPGDKPKIQEVKEORV 1070  
  
 RESULT 10  
 Q9UEY4  
 ID Q9UEY4 PRELIMINARY; PRT; 1227 AA.  
 AC Q9UEY4  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Anion exchanger 2 type b1.  
 GN SLC4A2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97179202; PubMed=9027488;  
 RA Medina J.F., Acin A., Prieto J.;  
 RT "Tissue-specific N-terminal isoforms from overlapping alternate  
 RL promoters of the human AE2 anion exchanger gene.";  
 DR Biochem. Biophys. Res. Commun. 267:228-235(2000).  
 DR EMBL; U76669; AAF19584.2; -;  
 DR EMBL; U76667; AAF19584.2; JOINED.  
 DR HSSP; P02730; 1BTO.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1227 AA; 135577 MW; 5D47714C17FB8EF7 CRC64;  
  
 Query Match 60.4%; Score 58; DB 13; Length 1219;  
 Best Local Similarity 63.2%; Pred. No. 1.6;  
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
 QY 2 KASTPGAAAOIQEVKEORI 20  
 DB 1052 KAVAPGDKPKIQEVKEORV 1070  
  
 RESULT 10  
 Q9UEY4  
 ID Q9UEY4 PRELIMINARY; PRT; 1227 AA.  
 AC Q9UEY4  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Anion exchanger 2 type b1.  
 GN SLC4A2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97179202; PubMed=9027488;  
 RA Medina J.F., Acin A., Prieto J.;  
 RT "Tissue-specific N-terminal isoforms from overlapping alternate  
 RL promoters of the human AE2 anion exchanger gene.";  
 DR Biochem. Biophys. Res. Commun. 267:228-235(2000).  
 DR EMBL; U76669; AAF19584.2; -;  
 DR EMBL; U76667; AAF19584.2; JOINED.  
 DR HSSP; P02730; 1BTO.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1227 AA; 135577 MW; 5D47714C17FB8EF7 CRC64;

Query Match 60.4%; Score 58; DB 4; Length 1227;  
 Best Local Similarity 63.2%; Pred. No. 1.6;  
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
 QY 2 KASTPGAAAOIQEVKEORI 20  
 DB 1059 KAVAPGDKPKIQEVKEORV 1077  
  
 RESULT 11  
 Q9UEY5  
 ID Q9UEY5 PRELIMINARY; PRT; 1232 AA.  
 AC Q9UEY5  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Anion exchanger 2 type b2.  
 GN SLC4A2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97179202; PubMed=9027488;  
 RA Medina J.F., Acin A., Prieto J.;  
 RT "Molecular cloning and characterization of the human AE2 anion  
 RL exchanger (SLC4A2) gene.";  
 DR Genomics 39:74-85(1997).  
 DR EMBL; U76669; AAF23240.1; -;  
 DR EMBL; U76667; AAF23240.1; JOINED.  
 DR HSSP; P02730; 1BTO.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1232 AA; 136218 MW; 22688C662907C2D7 CRC64;  
  
 Query Match 60.4%; Score 58; DB 4; Length 1232;  
 Best Local Similarity 63.2%; Pred. No. 1.6;  
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
  
 QY 2 KASTPGAAAOIQEVKEORI 20  
 DB 1064 KAVAPGDKPKIQEVKEORV 1082  
  
 RESULT 12  
 Q99654  
 ID Q99654 PRELIMINARY; PRT; 1241 AA.  
 AC Q99654  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE AE2 anion exchanger.  
 GN SLC4A2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]

SEQUENCE FROM N.A.  
 RX MEDLINE-97179202; PubMed-9027488;  
 RA Medina J.F., Acin A., Prieto J.;  
 RT "Molecular cloning and characterization of the human AE2 anion  
 RL exchanger (SLC4A2) gene.";  
 DR Genomics 39:74-85(1997).  
 DR EMBL; U62531; AAC50964.1; -.  
 DR HSSP; P02730; 1BTQ.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PRO1231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 1241 AA; 137009 MW; D266ECDAB238FD97 CRC64;

Query Match 60.4%; Score 58; DB 4; Length 1241;  
 Best Local Similarity 63.2%; Pred. No. 1.6;

Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KASTPGAAAIQIEVKQRI 20

DB 1073 KAVAFGDKPKIQIEVREQRV 1091

RESULT 13

Q9UEY6 PRELIMINARY; PRT; 1241 AA.

AC Q9UEY6;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anion exchanger 2 type a.  
 GN SLC4A2

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1] -

SEQUENCE FROM N.A.

RX MEDLINE-97179202; PubMed-9027488;

RA Medina J.F., Acin A., Prieto J.;  
 RT "Molecular cloning and characterization of the human AE2 anion  
 RL exchanger (SLC4A2) gene.";  
 DR Genomics 39:74-85(1997).  
 RN [2] -

SEQUENCE FROM N.A.

RX MEDLINE-20090621;  
 RA Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;  
 RT "Tissue-specific N-terminal isoforms from overlapping alternate  
 RT promoters of the human AE2 anion exchanger gene.";  
 RL Biochem. Biophys. Res. Commun. 267:228-235(2000).  
 DR EMBL; U76669; AAF19583.2; -.

DR EMBL; U76667; AAF19583.2; JOINED.

DR EMBL; U76668; AAF19583.2; JOINED.

DR HSSP; P02730; 1BTQ.

DR InterPro; IPR001717; Anion\_exchange.

DR InterPro; IPR003020; HCO3\_cotranspt.

DR Pfam; PF00955; HCO3\_cotransp; 1.

DR PRINTS; PRO1231; HCO3TRNSPORT.

DR TIGRFAMS; TIGR00834; ae; 1.

DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.

DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

SQ SEQUENCE 1241 AA; 136980 MW; D2FDA72E20D70D64 CRC64;

Query Match 60.4%; Score 58; DB 4; Length 1241;  
 Best Local Similarity 63.2%; Pred. No. 1.6;

Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KASTPGAAAIQIEVKQRI 20

DB 1073 KAVAFGDKPKIQIEVREQRV 1091

RESULT 14

Q99416 PRELIMINARY; PRT; 357 AA.

AC Q99416;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anion exchange protein (Fragment).  
 GN AE.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1] -

SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RA Gehrig H.H., Koenig J., Appelhans H.;

RT "Alternative anion exchange protein in human kidney.";

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; X87211; CAA60670.1; -.

DR InterPro; IPR001717; Anion\_exchange.

DR InterPro; IPR003020; HCO3\_cotranspt.

DR Pfam; PF00955; HCO3\_cotransp; 1.

DR PRINTS; PRO1231; HCO3TRNSPORT.

DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

FT NON\_TER 1

FT NON\_TER 357

SQ SEQUENCE 357 AA; 39526 MW; 40C03D49F3AF359C CRC64;

Query Match 56.2%; Score 54; DB 4; Length 357;  
 Best Local Similarity 61.1%; Pred. No. 1.9;

Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 ASTPGAAAIQIEVKQRI 20

DB 283 AIAPGDKPKIQIEVREQRV 300

RESULT 15

Q13717 PRELIMINARY; PRT; 357 AA.

AC Q13717;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Anion exchange protein 3 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1] -

SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RA Gehrig H., Appelhans H.;

RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.

DR EMBL; X70797; CAA50067.1; -.

DR InterPro; IPR001717; Anion\_exchange.

DR InterPro; IPR003020; HCO3\_cotranspt.

DR Pfam; PF00955; HCO3\_cotransp; 1.

DR PRINTS; PRO1231; HCO3TRNSPORT.

DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

FT NON\_TER 1

FT NON\_TER 357

SQ SEQUENCE 357 AA; 39544 MW; DCB1FA569E19EEF0 CRC64;

Query Match 56.2%; Score 54; DB 4; Length 357;  
 Best Local Similarity 61.1%; Pred. No. 1.9;

Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 ASTPGAAAIQIEVKQRI 20

DB 283 KAVAFGDKPKIQIEVREQRV 300

Db 283 AIAFGDKPQIQEVREQRV 300

Search completed: September 3, 2003, 11:50:04  
Job time : 45.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:24:37 ; Search time 48.5 Seconds  
(without alignments)  
65.454 Million cell updates/sec

Title: US-10-087-464-2  
Perfect score: 98  
Sequence: 1 SVTHANALTMKASTPGAA 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	20	23	AAE29340 Human Band 3 pepti
2	98	100.0	42	23	AAE29349 Human Band 3 prote
3	98	100.0	86	22	ABG54066 Human liver peptid
4	98	100.0	86	22	ABB39139 Peptide #6645 enco
5	98	100.0	86	22	ABB24030 Protein #6029 enco
6	98	100.0	86	22	AAW59792 Human brain expres
7	98	100.0	86	22	AAW72377 Human bone marrow
8	98	100.0	86	22	AAW32633 Peptide #6670 enco
9	98	100.0	86	23	ABG42195 Human peptide enco

10	98	100.0	911	12	AAAR15355 Human erythrocyte
11	98	100.0	911	20	AAW90263 A. tigrinum AE1 pr
12	98	100.0	911	22	AAAB46914 Human erythrocyte
13	98	100.0	911	23	AAE29343 Human Band 3 prote
14	98	100.0	911	23	AAE29344 Human Band 3 prote
15	98	100.0	962.	22	AAU30825 Novel human secret
16	73	74.5	292	7	AAAP60645 Mouse kidney cell
17	73	74.5	1240	20	AAW90262 A. tigrinum AE2 pr
18	61	62.2	1030	20	AAW90261 A. tigrinum AE3 pr
19	51	52.0	1239	22	ABB63733 Drosophila melanog
20	49	50.0	262	22	AAU35361 Haemophilus influe
21	49	50.0	262	22	AAAB88492 Haemophilus influe
22	49	50.0	262	23	AAU91423 Haemophilus influe
23	47	48.0	714	20	AAW74410 hNBC3 protein sequ
24	47	48.0	1032	20	AAW74409 hNBC3a protein sequ
25	47	48.0	1044	20	AAW74408 hNBC3 protein sequ
26	47	48.0	1044	21	AAW20659 Human brain-derive
27	47	48.0	1088	23	AAAB47931 Murine Nat-driven
28	47	48.0	1088	23	AAAB47932 Human Nat-driven C
29	47	48.0	1106	23	ABG32015 Human transporter
30	47	48.0	1129	23	ABG32014 Human transporter
31	47	48.0	1130	22	ABG03611 Novel human diagno
32	46	46.9	91	21	AAAB28321 Human secreted pro
33	46	46.9	93	21	AAAB28341 Human secreted pro
34	46	46.9	94	21	AAAB28342 Human secreted pro
35	46	46.9	860	22	AAAG91603 C glutamicum prote
36	46	46.9	971	21	AAAB11833 Human heart muscle
37	46	46.9	1000	20	AAW90274 Human NT2-2A prote
38	46	46.9	1267	11	AAAR04232 Rickettsia rickett
39	45	45.9	20	23	AAE29341 Human Band 3 pepti
40	44	44.9	20	23	AAE29339 Human Band 3 pepti
41	44	44.9	82	23	ABP05312 Human ORFX protein
42	44	44.9	154	22	AAAG81363 Human AFP protein
43	44	44.9	272	21	AAAB56872 Human prostate can
44	44	44.9	407	19	AAW74715 Amino acid sequenc
45	44	44.9	407	21	AAAY1558 A. orientalis gtfB

ALIGNMENTS

RESULT 1  
AAE29340  
ID AAE29340 standard; peptide; 20 AA.  
XX  
AC AAE29340;  
XX

DT 27-JAN-2003 (first entry)

XX Human Band 3 peptide, B35B.

DE Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;

KW protozoacide; gene therapy.

XX Homo sapiens.

XX WO200270542-A2.

PD 12-SEP-2002.

XX 01-MAR-2002; 2002WO-US06415.

XX 02-MAR-2001; 2001US-272930P.

XX (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX Chishtti AH, Oh SS, Liu D, Goel V;

XX WPI; 2002-759814/82.

XX New isolated Band 3 polypeptide which selectively binds to merozoite  
PT surface protein-1, useful for the prevention and treatment of malarial  
PT infection -

XX PS Claim 1; Page 84; 163pp; English.

XX CC The invention relates to an isolated Band 3 polypeptide that comprises  
CC any of 4 20 residue amino acid sequences, or their fragments that bind  
CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
CC pair sequences. The methods and compositions of the present invention  
CC are useful for the prevention and treatment of malarial infection. The  
CC present invention, develops new and more improved methods based upon  
CC inhibiting the particular interactions between the malarial parasite and  
CC a cognate molecule present in the host and subsequently minimising  
CC harmful side effects and drug resistance that may be due to non-specific  
CC therapeutic approaches. The invention is useful in gene therapy. The  
CC present invention also provides a vaccine for malaria. The present  
CC sequence is human Band 3 peptide.

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 98; DB 23; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SVTHANALTVMGKASTPGAA 20  
Db 1 SVTHANALTVMGKASTPGAA 20  
|||||

RESULT 2  
AAE29349  
ID AAE29349 standard; peptide; 42 AA.  
AC AAE29349;  
XX  
XX 27-JAN-2003 (first entry)  
DT Human Band 3 protein ectoplasmic domain 5.  
DE Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
KW protozoacide; gene therapy.  
KW Homo sapiens.  
XX OS  
XX WO200270542-A2.  
PN  
XX 12-SEP-2002.  
PD  
XX 01-MAR-2002; 2002WO-US06415.  
PF  
XX 02-MAR-2001; 2001US-272930P.  
PR (SELI-) ST ELIZABETH'S MEDICAL CENT INC.  
XX PA  
XX Chishti AH, Oh SS, Liu D, Goel V;  
PI  
XX WPI; 2002-759814/82.  
DR  
XX New isolated Band 3 polypeptide which selectively binds to merozoite  
PT surface protein-1, useful for the prevention and treatment of malarial  
PT infection -  
XX  
XX Example; Page 58; 163pp; English.

XX CC The invention relates to an isolated Band 3 polypeptide that comprises  
CC any of 4 20 residue amino acid sequences, or their fragments that bind  
CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
CC pair sequences. The methods and compositions of the present invention  
CC are useful for the prevention and treatment of malarial infection. The  
CC present invention, develops new and more improved methods based upon  
CC inhibiting the particular interactions between the malarial parasite and  
CC a cognate molecule present in the host and subsequently minimising  
CC harmful side effects and drug resistance that may be due to non-specific  
CC therapeutic approaches. The invention is useful in gene therapy. The  
CC present invention also provides a vaccine for malaria. The present  
CC sequence is human Band 3 peptide.

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 98; DB 23; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SVTHANALTVMGKASTPGAA 20  
Db 1 SVTHANALTVMGKASTPGAA 20  
|||||

RESULT 3  
ABG54066  
ID ABG54066 standard; peptide; 86 AA.  
XX  
AC ABG54066;  
XX  
XX 25-FEB-2003 (first entry)  
DT Human liver peptide, SEQ ID No 32714.  
DE  
DE Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KW hypercholesterolaemia; coronary heart disease.  
KW Homo sapiens.  
XX OS  
XX WO200157273-A2.  
PN  
XX 09-AUG-2001.  
PD  
XX 30-JAN-2001; 2001WO-US00664.  
PF  
XX 04-FEB-2000; 2000US-0180312.  
PR  
XX 26-MAY-2000; 2000US-0207456.  
PR  
XX 30-JUN-2000; 2000US-0608408.  
PR  
XX 03-AUG-2000; 2000US-0632366.  
PR  
XX 21-SEP-2000; 2000US-0234687.  
PR  
XX 27-SEP-2000; 2000US-0236359.  
PR  
XX 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-488898/53.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analysing gene expression in human adult liver -  
XX  
XX Claim 27; SEQ ID No 32714; 658pp; English.

XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult  
CC liver. (I) may be used for predicting, measuring and displaying gene  
CC expression in samples derived from human adult liver. The genes  
CC identified may be involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which  
CC is associated with coronary heart disease. ABG47348-ABG59930 represent  
CC human liver single exon encoded peptides of the invention.  
CC Note: The sequence information for this patent does not appear in the  
CC printed specification but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 86 AA;

Query Match 100.0%; Score 98; DB 22; Length 86;  
Best Local Similarity 100.0%; Pred. No. 8.4e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVTHANALTVMGKASTPGAA 20  
 Db 45 SVTHANALTVMGKASTPGAA 64

RESULT 4  
 ABB39139  
 ID ABB39139 standard; Peptide; 86 AA.  
 AC ABB39139;  
 DT 04-FEB-2002 (first entry)  
 DE Peptide #6645 encoded by human foetal liver single exon probe.  
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
 OS Homo sapiens.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PF 30-JAN-2001; 2001WO-US00669.  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI; 2001-483447/52.  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human fetal liver -  
 PS Claim 27; SEQ ID NO 31774; 639pp + sequence listing; English.  
 CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 SQ Sequence 86 AA;  
 Query Match 100.0%; Score 98; DB 22; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVTHANALTVMGKASTPGAA 20  
 Db 45 SVTHANALTVMGKASTPGAA 64

RESULT 5  
 ABB24030  
 ID ABB24030 standard; Protein; 86 AA.  
 AC ABB24030;  
 DT 23-JAN-2002 (first entry)

XX Protein #6029 encoded by probe for measuring heart cell gene expression.  
 DE Human; gene expression; heart; microarray; vascular system;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease.  
 XX Homo sapiens.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PF 30-JAN-2001; 2001WO-US00666.  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI; 2001-488899/53.  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts -  
 PS Claim 15; SEQ ID No 25800; 530pp; English.  
 CC The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart (see  
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
 CC probe. The probes may be used for predicting, measuring and displaying  
 CC gene expression in samples derived from the human heart via microarrays.  
 CC By measuring gene expression, the probes are useful for predicting,  
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
 CC human heart and vascular system e.g. cardiovascular disease,  
 CC hypertension, cardiac arrhythmias and congenital heart disease.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 SQ Sequence 86 AA;  
 Query Match 100.0%; Score 98; DB 22; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVTHANALTVMGKASTPGAA 20  
 Db 45 SVTHANALTVMGKASTPGAA 64

RESULT 6  
 AAM59792  
 ID AAM59792 standard; Protein; 86 AA.  
 AC AAM59792;  
 DT 05-NOV-2001 (first entry)  
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.  
 KW Human; brain expressed exon; gene expression analysis; probe;  
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
 KW epilepsy; cancer.  
 OS Homo sapiens.

```
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483446/52.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains -
XX PS Example 4; SEQ ID NO: 31897; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention.
XX SQ Sequence 86 AA;
XX Query Match 100.0%; Score 98; DB 22; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 8.4e-09;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SVTHANALTVMGKASTPGAA 20
XX DB 45 SVTHANALTVMGKASTPGAA 64
XX RESULT 7
XX AAM72377
XX ID AAM72377 standard; Protein; 86 AA.
XX AC AAM72377;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32683.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
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XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488900/53.
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human bone marrow -
XX PS Example 4; SEQ ID NO: 32683; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention.
XX SQ Sequence 86 AA;
XX Query Match 100.0%; Score 98; DB 22; Length 86;
XX Best Local Similarity 100.0%; Pred. No. 8.4e-09;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 SVTHANALTVMGKASTPGAA 20
XX DB 45 SVTHANALTVMGKASTPGAA 64
XX RESULT 8
XX AAM32633
XX ID AAM32633 standard; Protein; 86 AA.
XX AC AAM32633;
XX DT 17-OCT-2001 (first entry)
XX DE Peptide #6670 encoded by probe for measuring placental gene expression.
XX KW Probe: microarray; human; placenta; antenatal diagnosis;
XX KW genetic disorder.
XX OS Homo sapiens.
XX PN WO200157272-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000663.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488897/53.
XX PT Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human placenta -
XX PS Claim 27; SEQ ID NO 32902; 654pp; English.
XX CC The present invention relates to single exon nucleic acid probes (SENP:
XX CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
XX CC such probe. The probes are useful for producing a microarray for
```

CC predicting, measuring and displaying gene expression in samples derived  
 CC from human placenta. The probes are useful for antenatal diagnosis of  
 CC human genetic disorders.

XX Sequence 86 AA;

Query Match 100.0%; Score 98; DB 22; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPGAA 20  
 Db 45 SVTHANALTMVGKASTPGAA 64

RESULT 9

ID ABG42195 standard; Peptide; 86 AA.

AC ABG42195;

XX 19-AUG-2002 (first entry)

DE Human peptide encoded by genome-derived single exon probe SEQ ID 31860.

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW primary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.

XX Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US00665.

XX 04-FEB-2000; 2000US-180312P.

PR 26-MAY-2000; 2000US-207456P.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0623266.

PR 21-SEP-2000; 2000US-234687P.

PR 27-SEP-2000; 2000US-236359P.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples -

XX Claim 27; SEQ ID No 31860; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of  
 CC probes; the novel set of probes which hybridise at high stringency to a  
 CC nucleic acid expressed in the human lung; measuring gene expression in a  
 CC sample derived from human lung, comprising (a) contacting the array with  
 CC a collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of

CC the array; identifying exons in a eukaryotic genome, comprising  
 CC (a) algorithmically predicting at least one exon from genomic sequences  
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene  
 CC expression analysis, and for identifying exons in a gene, particularly  
 CC using human lung derived mRNA and for the study of lung diseases  
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
 CC and hyaline membrane disease. The present sequence is a peptide/protein  
 CC encoded by a single exon probe of the invention.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 86 AA;

Query Match 100.0%; Score 98; DB 23; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPGAA 20  
 Db 45 SVTHANALTMVGKASTPGAA 64

RESULT 10

AAR15355

ID AAR15355 standard; Protein; 911 AA.

AC AAR15355;

XX 25-MAR-2003 (updated)

DT 08-MAR-1992 (first entry)

XX Human erythrocyte membrane anion-transport protein (band 3).

XX Senescent cell peptide; ANION 1; COOH; auto immune disease.

XX Homo sapiens.

XX WO9118013-A.

XX 28-NOV-1991.

XX 24-MAY-1991; 91WO-US03557.

XX 24-MAY-1990; 90US-0528210.

XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.

XX Kay MBM, Marchalonis JJ;

XX WPI; 1991-369184/50.

XX N-PSDB; AAQ15172.

XX Synthetic senescent cell antigen and peptide(s) - used to detect  
 PT antibodies to SCA, study cellular ageing and auto-immune



CC physiological effect of a composition comprising hemoglobin which  
 CC involves obtaining electron paramagnetic resonance (EPR) or UV spectra of  
 CC iron-nitrosyl hemoglobin derivatives formed by incubation of limiting  
 CC nitric oxide (NO) with hemoglobin and determining if the composition  
 CC shows non-cooperativity or cooperativity in binding of NO to the  
 CC hemoglobin. The products of the invention have antianemic; antibacterial;  
 CC immunosuppressive; vasotropic; antiinflammatory; antiasthmatic;  
 CC respiratory; antiarthritic and cerebroprotective activity. The products  
 CC of the invention are used to produce methods of therapy for medical  
 CC disorders characterized by red blood cell membrane defects and for a  
 CC variety of hypercoagulable and vasculopathic states, particularly for  
 CC patients with septic shock who develop myocardial depression,  
 CC pancreatitis and progressive respiratory failure, patients with  
 CC septicemia as a complication of urinary tract infection and patients with  
 CC ischemia, patients in a sickle cell crisis and for treating inflammatory  
 CC conditions such as arthritis, asthma, cerebritis, bronchitis and  
 CC vasculitis. The methods are also used for preserving red blood cells  
 CC which can be used in therapy.

XX Sequence 911 AA;  
 Query Match 100.0%; Score 98; DB 22; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVTHANALVTMGKASTPGAA 20  
 Db 731 SVTHANALVTMGKASTPGAA 750  
 |||||

RESULT 13  
 AAE29343  
 ID AAE29343 standard; Protein; 911 AA.

XX AC AAE29343;  
 XX DT 27-JAN-2003 (first entry)  
 XX DE Human Band 3 protein #1.  
 XX KW Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
 KW protozoacide; gene therapy.

XX OS Homo sapiens.

XX PN WO200270542-A2.

XX PD 12-SEP-2002.

XX PF 01-MAR-2002; 2002WO-US06415.

XX PR 02-MAR-2001; 2001US-272930P.

XX PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX PI Chishti AH, Oh SS, Liu D, Goel V;

XX DR N-PSDB; AAD46978.

XX WPI; 2002-759814/82.

PT New isolated Band 3 polypeptide which selectively binds to merozoite  
 PT surface protein-1, useful for the prevention and treatment of malarial  
 PT infection -

XX PS Disclosure; Page 102-105; 163pp; English.

XX The invention relates to an isolated Band 3 polypeptide that comprises  
 CC any of 4 20 residue amino acid sequences, or their fragments that bind  
 CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
 CC pair sequences. The methods and compositions of the present invention  
 CC are useful for the prevention and treatment of malarial infection. The  
 CC present invention, develops new and more improved methods based upon  
 CC inhibiting the particular interactions between the malarial parasite and

CC a cognate molecule present in the host and subsequently minimizing  
 CC harmful side effects and drug resistance that may be due to non-specific  
 CC therapeutic approaches. The invention is useful in gene therapy. The  
 CC present invention also provides a vaccine for malaria. The present  
 CC sequence is human Band 3 protein.

XX Sequence 911 AA;

Query Match 100.0%; Score 98; DB 23; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVTHANALVTMGKASTPGAA 20  
 Db 731 SVTHANALVTMGKASTPGAA 750  
 |||||

RESULT 14  
 AAE29344  
 ID AAE29344 standard; Protein; 911 AA.

XX AC AAE29344;

XX DT 27-JAN-2003 (first entry)

XX DE Human Band 3 protein #2.

XX KW Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
 KW protozoacide; gene therapy.

XX OS Homo sapiens.

XX PN WO200270542-A2.

XX PD 12-SEP-2002.

XX PF 01-MAR-2002; 2002WO-US06415.

XX PR 02-MAR-2001; 2001US-272930P.

XX PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX PI Chishti AH, Oh SS, Liu D, Goel V;

XX WPI; 2002-759814/82.

XX DR N-PSDB; AAD46979.

PT New isolated Band 3 polypeptide which selectively binds to merozoite  
 PT surface protein-1, useful for the prevention and treatment of malarial  
 PT infection -

XX PS Disclosure; Page 107-110; 163pp; English.

XX The invention relates to an isolated Band 3 polypeptide that comprises  
 CC any of 4 20 residue amino acid sequences, or their fragments that bind  
 CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
 CC pair sequences. The methods and compositions of the present invention  
 CC are useful for the prevention and treatment of malarial infection. The  
 CC present invention, develops new and more improved methods based upon  
 CC inhibiting the particular interactions between the malarial parasite and  
 CC a cognate molecule present in the host and subsequently minimizing  
 CC harmful side effects and drug resistance that may be due to non-specific  
 CC therapeutic approaches. The invention is useful in gene therapy. The  
 CC present invention also provides a vaccine for malaria. The present  
 CC sequence is human Band 3 protein.

XX Sequence 911 AA;

Query Match 100.0%; Score 98; DB 23; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVTHANALVTMGKASTPGAA 20

```

Db      731 SVTHANALTVMGKASTPGAA 750
|||||
RESULT 15
AAU30825
ID AU30825 standard; Protein; 962 AA.
XX
AC AU30825;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #1316.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN W0200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
XX
PT 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX
PS Claim 20; Page 354; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 962 AA;
Query Match 100.0%; Score 98; DB 22; Length 962;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVTHANALTVMGKASTPGAA 20
|||||
Db 782 SVTHANALTVMGKASTPGAA 801

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Search completed: September 3, 2003, 11:46:11  
 Job time : 48.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:24:37 ; Search time 48.5 Seconds  
(without alignments)  
65.454 Million cell updates/sec

Title: US-10-087-464-3

Perfect score: 96

Sequence: 1 GKASTGAAAOIEVKEQRI 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	96	100.0	20	23	AAE29341		Human Band 3 pepti
2	96	100.0	42	23	AAE29349		Human Band 3 prote
3	96	100.0	86	22	ABG54066		Human liver peptid
4	96	100.0	86	22	ABB39139		Peptide #6645 enco
5	96	100.0	86	22	ABB24030		Protein #6029 enco
6	96	100.0	86	22	AAAS59792		Human brain expres
7	96	100.0	86	22	AAW72377		Human bone marrow
8	96	100.0	86	22	AAW32633		Peptide #6670 enco
9	96	100.0	86	23	ABG42195		Human peptide enco

10	96	100.0	911	12	AAE15355	Human erythrocyte
11	96	100.0	911	20	AAW90263	A. tigrinum AE1 pr
12	96	100.0	911	22	AAW46914	Human erythrocyte
13	96	100.0	911	23	AAE29343	Human Band 3 prote
14	96	100.0	911	23	AAE29344	Human Band 3 prote
15	96	100.0	962	22	AAU30825	Novel human secret
16	58	60.4	292	7	AAE60645	Mouse kidney cell
17	58	60.4	1240	20	AAW90262	A. tigrinum AE2 pr
18	54	56.2	1030	20	AAW90261	A. tigrinum AE3 pr
19	45	46.9	20	23	AAE29340	Human Band 3 pepti
20	45	46.9	172	22	ABG11308	Novel human diagno
21	45	46.9	391	22	ABG67472	Amino acid sequenc
22	45	46.9	1253	22	ABB60494	Drosophila melanog
23	44	45.8	1837	22	ABB62913	Drosophila melanog
24	44	45.8	220	23	AAU78292	Human Pregnane X R
25	44	45.8	300	22	AAU07094	Human odorant rece
26	44	45.8	455	15	AAE57771	Mouse nucleobindin
27	44	45.8	460	15	AAE49667	Human nucleobindin
28	44	45.8	1239	22	ABB63733	Drosophila melanog
29	44	45.8	3816	21	AAE92708	S. antibioticus 8,
30	43	44.8	62	21	AAE02687	Human secreted pro
31	43	44.8	264	21	AAE06500	Arabidopsis thalia
32	43	44.8	269	21	AAE06499	Arabidopsis thalia
33	43	44.8	323	21	AAE06498	Arabidopsis thalia
34	43	44.8	1162	22	ABG09158	Novel human diagno
35	43	44.8	1857	21	AAE33970	Human ORFX protein
36	42	43.8	76	23	ABP03958	Human ORFX protein
37	42	43.8	116	22	AAE06600	Human polypeptide
38	42	43.8	296	23	ABP28318	Streptococcus poly
39	42	43.8	1492	22	ABG14001	Novel human diagno
40	42	43.8	2379	23	ABP62760	S. roseosporus dap
41	42	43.8	3238	22	ABB71715	Drosophila melanog
42	41	42.7	81	21	AAE37475	Arabidopsis thalia
43	41	42.7	85	21	AAE37474	Arabidopsis thalia
44	41	42.7	99	21	AAE37473	Arabidopsis thalia
45	41	42.7	114	22	ABB95927	Human testicular a

#### ALIGNMENTS

RESULT 1  
AAE29341  
ID AAE29341 standard; peptide; 20 AA.  
XX  
AC AAE29341;  
XX  
DT 27-JAN-2003 (first entry)  
XX  
DE Human Band 3 peptide, B35C.  
XX  
KW Human: Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
KW protozoacide; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200270542-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 01-MAR-2002; 2002WO-US06415.  
XX  
PR 02-MAR-2001; 2001US-272930P.  
XX  
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.  
XX  
PI Chisht AH, Oh SS, Liu D, Goel V;  
XX  
DR WPI; 2002-759814/82.  
XX  
PT New isolated Band 3 polypeptide which selectively binds to merozoite  
PT surface protein-1, useful for the prevention and treatment of malarial  
infection

XX Claim 1; Page 84; 163pp; English.

XX The invention relates to an isolated Band 3 polypeptide that comprises

CC any of 4 20 residue amino acid sequences, or their fragments that bind

CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base

CC pair sequences. The methods and compositions of the present invention

CC are useful for the prevention and treatment of malarial infection. The

CC present invention, develops new and more improved methods based upon

CC inhibiting the particular interactions between the malarial parasite and

CC a cognate molecule present in the host and subsequently minimising

CC harmful side effects and drug resistance that may be due to non-specific

CC therapeutic approaches. The invention is useful in gene therapy. The

CC present invention also provides a vaccine for malaria. The present

CC sequence is human Band 3 peptide.

XX Sequence 20 AA;

XX Query Match 100.0%; Score 96; DB 23; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.4e-09;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAAQIOEVKEQRI 20

DB 1 GKASTPGAAAQIOEVKEQRI 20

RESULT 2

AAE29349

ID AAE29349 standard; peptide; 42 AA.

XX AAE29349;

XX 27-JAN-2003 (first entry)

XX Human Band 3 protein ectoplasmic domain 5.

XX Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;

KW protozoacide; gene therapy.

XX Homo sapiens.

XX WO200270542-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002WO-US06415.

XX 02-MAR-2001; 2001US-272930P.

XX (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX Chishti AH, Oh SS, Liu D, Goel V;

XX WPI; 2002-759814/82.

XX New isolated Band 3 polypeptide which selectively binds to merozoite

PT surface protein-1, useful for the prevention and treatment of malarial

PT infection

XX Example; Page 58; 163pp; English.

XX The invention relates to an isolated Band 3 polypeptide that comprises

CC any of 4 20 residue amino acid sequences, or their fragments that bind

CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base

CC pair sequences. The methods and compositions of the present invention

CC are useful for the prevention and treatment of malarial infection. The

CC present invention, develops new and more improved methods based upon

CC inhibiting the particular interactions between the malarial parasite and

CC a cognate molecule present in the host and subsequently minimising

CC harmful side effects and drug resistance that may be due to non-specific

CC therapeutic approaches. The invention is useful in gene therapy. The

CC present invention also provides a vaccine for malaria. The present

CC sequence is human Band 3 protein ectoplasmic domain 5.

XX Sequence 42 AA;

XX Query Match 100.0%; Score 96; DB 23; Length 42;

XX Best Local Similarity 100.0%; Pred. No. 5.6e-09;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAAQIOEVKEQRI 20

DB 23 GKASTPGAAAQIOEVKEQRI 42

RESULT 3

ABG54066

ID ABG54066 standard; Peptide; 86 AA.

XX ABG54066;

XX 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID No 32714.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;

KW hypercholesterolaemia; coronary heart disease.

XX Homo sapiens.

XX WO200157273-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00664.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for

PT analysing gene expression in human adult liver

XX Claim 27; SEQ ID No 32714; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for

CC measuring human gene expression in a sample derived from human adult

CC liver, comprising one of 13109 defined nucleotide sequences given in the

CC specification (or complements/ fragments). The probe hybridises at high

CC stringency to a nucleic acid molecule expressed in the human adult

CC liver. (I) may be used for predicting, measuring and displaying gene

CC expression in samples derived from human adult liver. The genes

CC identified may be involved in genetic liver diseases such as cirrhosis,

CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which

CC is associated with coronary heart disease. ABG47348-ABG59930 represent

CC human liver single exon encoded peptides of the invention.

CC Note: The sequence information for this patent does not appear in the

CC printed specification but was obtained in electronic format directly

CC from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

XX Sequence 86 AA;

XX Query Match 100.0%; Score 96; DB 22; Length 86;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-08;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GKASTPGAAQIQEVKEQRI 20
   |||||
Db 56 GKASTPGAAQIQEVKEQRI 75

RESULT 4
ABB39139
ID ABB39139 standard; Peptide; 86 AA.
XX
AC ABB39139;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #6645 encoded by human foetal liver single exon probe.
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human foetal liver -
XX
PS Claim 27; SEQ ID NO 31774; 639pp + sequence listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC foetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO.int/pub/published_pct_sequences.
XX
SQ Sequence 86 AA;

Query Match 100.0%; Score 96; DB 22; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAQIQEVKEQRI 20
   |||||
Db 56 GKASTPGAAQIQEVKEQRI 75

RESULT 5
ABB24030
ID ABB24030 standard; Protein; 86 AA.
XX
AC ABB24030;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.
KW Human; brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX
OS Homo sapiens.

```

---

```

XX DE 1 GKASTPGAAQIQEVKEQRI 20
XX |||||
KW KW Human; gene expression; heart; microarray; vascular system;
KW KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW KW congenital heart disease.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00666.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488899/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts -
XX PS Claim 15; SEQ ID No 25800; 530pp; English.
XX CC The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart (see
XX CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX CC probe. The probes may be used for predicting, measuring and displaying
XX CC gene expression in samples derived from the human heart via microarrays.
XX CC By measuring gene expression, the probes are useful for predicting,
XX CC diagnosing, grading, staging, monitoring and prognosing diseases of the
XX CC human heart and vascular system e.g. cardiovascular disease,
XX CC hypertension, cardiac arrhythmias and congenital heart disease.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 86 AA;

Query Match 100.0%; Score 96; DB 22; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAQIQEVKEQRI 20
   |||||
Db 56 GKASTPGAAQIQEVKEQRI 75

RESULT 6
AAM59792
ID AAM59792 standard; Protein; 86 AA.
XX
AC AAM59792;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.
KW Human; brain expressed exon; gene expression analysis; probe;
KW KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW KW epilepsy; cancer.
XX
OS Homo sapiens.

```

XX WO200157275-A2.  
 XX  
 XX  
 XX PD 09-AUG-2001.  
 XX  
 XX PF 30-JAN-2001; 2001WO-US00667.  
 XX  
 XX PR 04-FEB-2000; 2000US-0180312.  
 XX PR 26-MAY-2000; 2000US-0207456.  
 XX PR 30-JUN-2000; 2000US-0608408.  
 XX PR 03-AUG-2000; 2000US-0632366.  
 XX PR 21-SEP-2000; 2000US-0234687.  
 XX PR 27-SEP-2000; 2000US-0236359.  
 XX PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DX WPI; 2001-483446/52.  
 XX  
 XX Single exon nucleic acid probes for analyzing gene expression in human brains -  
 XX  
 XX PS Example 4; SEQ ID NO: 31897; 650pp + Sequence Listing; English.  
 XX  
 XX CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.

XX SQ Sequence 86 AA;

Query Match 100.0%; Score 96; DB 22; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRASTPGAAAIQIYEKQRI 20  
 |||||

DB 56 GRASTPGAAAIQIYEKQRI 75  
 |||||

RESULT 7  
 AAM72377  
 ID AAM72377 standard; Protein; 86 AA.  
 XX  
 XX AC AAM72377;  
 XX DT 06-NOV-2001 (first entry)  
 XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32683.  
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe;  
 XX KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 XX OS Homo sapiens.  
 XX PN WO200157276-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US00668.  
 XX PR 04-FEB-2000; 2000US-0180312.  
 XX PR 26-MAY-2000; 2000US-0207456.  
 XX PR 30-JUN-2000; 2000US-0608408.  
 XX PR 03-AUG-2000; 2000US-0632366.  
 XX PR 21-SEP-2000; 2000US-0234687.  
 XX PR 27-SEP-2000; 2000US-0236359.  
 XX PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DX WPI; 2001-488897/53.  
 XX  
 XX Single exon nucleic acid probes for analyzing gene expression in human placenta -  
 XX  
 XX PS Claim 27; SEQ ID No 32902; 654pp; English.  
 XX  
 XX CC The present invention relates to single exon nucleic acid probes (SENPs:  
 see AA131315-AA157546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for

XX SQ Sequence 86 AA;

Query Match 100.0%; Score 96; DB 22; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRASTPGAAAIQIYEKQRI 20  
 |||||

DB 56 GRASTPGAAAIQIYEKQRI 75  
 |||||

RESULT 8  
 AAM32633  
 ID AAM32633 standard; Protein; 86 AA.  
 XX  
 XX AC AAM32633;  
 XX DT 17-OCT-2001 (first entry)  
 XX DE Peptide #6670 encoded by probe for measuring placental gene expression.  
 XX KW Probe; microarray; human; placenta; antenatal diagnosis;  
 XX KW genetic disorder.  
 XX OS Homo sapiens.  
 XX PN WO200157272-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US00663.  
 XX PR 04-FEB-2000; 2000US-0180312.  
 XX PR 26-MAY-2000; 2000US-0207456.  
 XX PR 30-JUN-2000; 2000US-0608408.  
 XX PR 03-AUG-2000; 2000US-0632366.  
 XX PR 21-SEP-2000; 2000US-0234687.  
 XX PR 27-SEP-2000; 2000US-0236359.  
 XX PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DX WPI; 2001-488897/53.  
 XX  
 XX Single exon nucleic acid probes for analyzing gene expression in human placenta -  
 XX  
 XX PS Claim 27; SEQ ID No 32902; 654pp; English.  
 XX  
 XX CC The present invention relates to single exon nucleic acid probes (SENPs:  
 see AA131315-AA157546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for

XX SQ Sequence 86 AA;

Query Match 100.0%; Score 96; DB 22; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRASTPGAAAIQIYEKQRI 20  
 |||||

DB 56 GRASTPGAAAIQIYEKQRI 75  
 |||||

RESULT 7  
 AAM72377  
 ID AAM72377 standard; Protein; 86 AA.  
 XX  
 XX AC AAM72377;  
 XX DT 06-NOV-2001 (first entry)  
 XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32683.  
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe;  
 XX KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 XX OS Homo sapiens.  
 XX PN WO200157276-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US00668.  
 XX PR 04-FEB-2000; 2000US-0180312.  
 XX PR 26-MAY-2000; 2000US-0207456.  
 XX PR 30-JUN-2000; 2000US-0608408.  
 XX PR 03-AUG-2000; 2000US-0632366.  
 XX PR 21-SEP-2000; 2000US-0234687.  
 XX PR 27-SEP-2000; 2000US-0236359.  
 XX PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DX WPI; 2001-488897/53.  
 XX  
 XX Single exon nucleic acid probes for analyzing gene expression in human placenta -  
 XX  
 XX PS Claim 27; SEQ ID No 32902; 654pp; English.  
 XX  
 XX CC The present invention relates to single exon nucleic acid probes (SENPs:  
 see AA131315-AA157546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for

XX SQ Sequence 86 AA;

Query Match 100.0%; Score 96; DB 22; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRASTPGAAAIQIYEKQRI 20  
 |||||

DB 56 GRASTPGAAAIQIYEKQRI 75  
 |||||

RESULT 8  
 AAM32633  
 ID AAM32633 standard; Protein; 86 AA.  
 XX  
 XX AC AAM32633;  
 XX DT 17-OCT-2001 (first entry)  
 XX DE Peptide #6670 encoded by probe for measuring placental gene expression.  
 XX KW Probe; microarray; human; placenta; antenatal diagnosis;  
 XX KW genetic disorder.  
 XX OS Homo sapiens.  
 XX PN WO200157272-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US00663.  
 XX PR 04-FEB-2000; 2000US-0180312.  
 XX PR 26-MAY-2000; 2000US-0207456.  
 XX PR 30-JUN-2000; 2000US-0608408.  
 XX PR 03-AUG-2000; 2000US-0632366.  
 XX PR 21-SEP-2000; 2000US-0234687.  
 XX PR 27-SEP-2000; 2000US-0236359.  
 XX PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DX WPI; 2001-488897/53.  
 XX  
 XX Single exon nucleic acid probes for analyzing gene expression in human placenta -  
 XX  
 XX PS Claim 27; SEQ ID No 32902; 654pp; English.  
 XX  
 XX CC The present invention relates to single exon nucleic acid probes (SENPs:  
 see AA131315-AA157546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for

XX SQ Sequence 86 AA;

Query Match 100.0%; Score 96; DB 22; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRASTPGAAAIQIYEKQRI 20  
 |||||

DB 56 GRASTPGAAAIQIYEKQRI 75  
 |||||

RESULT 8  
 AAM32633  
 ID AAM32633 standard; Protein; 86 AA.  
 XX  
 XX AC AAM32633;  
 XX DT 17-OCT-2001 (first entry)  
 XX DE Peptide #6670 encoded by probe for measuring placental gene expression.  
 XX KW Probe; microarray; human; placenta; antenatal diagnosis;  
 XX KW genetic disorder.  
 XX OS Homo sapiens.  
 XX PN WO200157272-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001

CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders.

XX Sequence 86 AA;  
SQ

Query Match 100.0%; Score 96; DB 22; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAQIQEVKEQRI 20  
Db 56 GKASTPGAAQIQEVKEQRI 75

RESULT 9  
ABG42195  
ID ABG42195 standard; Peptide; 86 AA.  
XX  
AC ABG42195;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 31860.  
XX  
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.

XX Homo sapiens.  
XX  
XX WO200186003-A2.  
XX  
XX 15-NOV-2001.  
XX  
XX 30-JAN-2001; 2001WO-US00665.  
XX  
XX 04-FEB-2000; 2000US-180312P.  
XX PR 26-MAY-2000; 2000US-207456P.  
XX PR 30-JUN-2000; 2000US-0608408.  
XX PR 03-AUG-2000; 2000US-0632366.  
XX PR 21-SEP-2000; 2000US-234687P.  
XX PR 27-SEP-2000; 2000US-236359P.  
XX PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2002-114183/15.  
XX  
XX Spatially-addressable set of single exon nucleic acid probes, used to  
XX measure gene expression in human lung samples -  
XX  
XX Claim 27; SEQ ID No 31860; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon  
XX nucleic acid probes for measuring gene expression in a sample derived  
XX from human lung comprising single exon nucleic acid probes having one of  
XX 12614 nucleic acid sequences mentioned in the specification, or their  
XX complements or the 12387 open reading frames derived from the 12614  
XX probes. Also included are a microarray comprising the novel set of  
XX probes; the novel set of probes which hybridise at high stringency to a  
XX nucleic acid expressed in the human lung; measuring gene expression in a  
XX sample derived from human lung, comprising (a) contacting the array with  
XX a collection of detectably labeled nucleic acids derived from human lung  
XX mRNA, and (b) measuring the label detectably bound to each probe of

CC the array; identifying exons in a eukaryotic genome, comprising  
CC (a) algorithmically predicting at least one exon from genomic sequences  
CC of the eukaryote; and (b) detecting specific hybridisation of detectably  
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene  
CC expression analysis, and for identifying exons in a gene, particularly  
CC using human lung derived mRNA and for the study of lung diseases  
CC such as asthma, lung cancer, chronic obstructive pulmonary disease  
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic  
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
CC and hyaline membrane disease. The present sequence is a peptide/protein  
CC encoded by a single exon probe of the invention.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 86 AA;

Query Match 100.0%; Score 96; DB 23; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.3e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAQIQEVKEQRI 20  
Db 56 GKASTPGAAQIQEVKEQRI 75

RESULT 10

AAR15355  
ID AAR15355 standard; Protein; 911 AA.

XX  
AC AAR15355;

XX 25-MAR-2003 (updated)

DT 08-MAR-1992 (first entry)

XX Human erythrocyte membrane anion-transport protein (band 3).

XX Senescent cell peptide; ANION 1; COOH; auto immune disease.

XX Homo sapiens.

XX WO9118013-A.

XX 28-NOV-1991.

XX 24-MAY-1991; 91WO-US03557.

XX 24-MAY-1990; 90US-0528210.

XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.

XX Kay MBM, Marchalonis JJ;

XX WPI; 1991-369184/50.

XX N-PSDB; AAQ15172.

XX Synthetic senescent cell antigen and peptide(s) - used to detect  
XX antibodies to SCA, study cellular ageing and auto-immune

PT mechanisms, separate anions and treat auto-immune disease  
 XX Disclosure; Fig 1; 74pp; English.  
 XX The amino acid sequence is that of the human erythrocyte anion-transport  
 CC protein (band 3). Amino acids 538-554 (ANION 1) or 812-827 (COOH) code  
 CC for a peptide which is immuno-reactive with antibodies to senescent cell  
 CC antigen (SCA). The antigen and peptides can be used in any method or  
 CC technique involving or requiring the inhibition of the binding of  
 CC senescent cell IgG to senescent cells in vitro or in vivo. The prods.  
 CC can be used in to examine various physiological, biochemical, and  
 CC immunological mechanisms in humans and other animals, such as those  
 CC relating to cellular ageing, degeneration, and life span; removal of  
 CC senescent cells; anion transport across cellular membranes; disease  
 CC mechanisms where increased senescent cell IgG may play a role, such  
 CC as haemolytic anaemia, sickle cell anaemia, and idiopathic  
 CC thrombocytopenia purpura; other autoimmune disease mechanisms, such  
 CC as rheumatoid arthritis and systemic lupus erythematosus; and other  
 CC diseases such as those involved in malaria and cancer. More  
 CC specifically, the prods. are useful in cosmetic and pharmaceutical  
 CC compns., diagnostic kits, and methods for detecting or measuring  
 CC Abs to SCA, studying cellular ageing and autoimmune mechanisms,  
 CC separating anions from a gas or liquid, or diagnosis and treatment  
 CC of certain diseases.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX Sequence 911 AA;  
 SQ

Query Match 100.0%; Score 96; DB 12; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRASTPGAAQIQEVKEQRI 20  
 DB 742 GRASTPGAAQIQEVKEQRI 761  
 |||||

RESULT 11  
 AAW90263  
 ID AAW90263 standard; peptide; 911 AA.  
 XX AAW90263;  
 XX  
 DT 27-APR-1999 (first entry)  
 XX  
 DE A. tigrinum AEL protein.  
 XX  
 KW NBC; sodium bicarbonate transporter family; pH regulation; immunoassay;  
 KW treatment; water retention; blood pressure; acidosis; inflammation;  
 KW cell proliferation; cancer; sperm activation; inactivation; epilepsy;  
 KW hydroencephaly; glaucoma; colitis; salamander; AEL; anion exchange.  
 XX Ambystoma tigrinum.  
 OS  
 XX  
 XX  
 XX WO9853067-A1.  
 XX  
 XX 26-NOV-1998.  
 XX  
 XX 20-MAY-1998; 98WO-US10297.  
 XX  
 XX 20-MAY-1997; 97US-0047131.  
 XX  
 XX (UYUA) UNIV YALE.  
 XX  
 XX Aalkjaer C, Bevenssee MO, Biemesderfer D, Boron WF;  
 XX Choi I, Davis BA, Grichtchenko II, Romero MF, Schmitt BM;  
 XX Sussman CR;  
 XX WPI; 1999-059743/05.  
 XX  
 XX New nucleic acid molecules encoding proteins of the Sodium  
 PT Bicarbonate Cotransporter (NBC) family - useful for identifying  
 PT agents that agonise or antagonise NBC activity and treating

PT disorders mediated by NBC  
 XX  
 PS Example 1; Fig 5; 138pp; English.  
 XX  
 CC This sequence represents the anion exchange protein AEL which is used in  
 CC a method resulting in the isolation of a novel salamander sodium  
 CC bicarbonate transporter (NBC). NBC proteins and nucleic acid sequences  
 CC may be used to treat pathological processes including water retention,  
 CC increased blood pressure, chronic respiratory and metabolic acidosis,  
 CC inflammation, cell proliferation, cancer, sperm activation/inactivation,  
 CC hydroencephaly, epilepsy, glaucoma and colitis. Members of the NBC family  
 CC of proteins can be used (i) as a target to identify agents that block or  
 CC stimulate NBC mediated pH regulation, (ii) as a target or bait to  
 CC identify and isolate binding partners that bind NBC, (iii) in methods to  
 CC identify agents that block or stimulate activity of an NBC protein, and  
 CC (iv) as a target to assay for NBC-mediated activity. Anti-NBC antibodies  
 CC are also useful as modulators of NBC activity, useful in the immunoassays  
 CC for detecting NBC expression/activity and for purifying an NBC protein.  
 XX Sequence 911 AA;  
 SQ

Query Match 100.0%; Score 96; DB 20; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRASTPGAAQIQEVKEQRI 20  
 DB 742 GRASTPGAAQIQEVKEQRI 761  
 |||||

RESULT 12  
 AAB46914  
 ID AAB46914 standard; protein; 911 AA.  
 XX AAB46914;  
 XX  
 DT 04-MAY-2001 (first entry)  
 XX  
 DE Human erythrocyte band 3 anion transporter protein.  
 XX  
 KW Erythrocyte band 3 anion transporter protein; human; hypercoagulation;  
 KW iron-nitrosyl hemoglobin; electron paramagnetic resonance; UV spectra;  
 KW EPR; nitric oxide; antianemic; antibacterial; immunosuppressive;  
 KW vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic;  
 KW cerebroprotective; red blood cell membrane defect; vasculopathy;  
 KW septic shock myocardial depression; pancreatitis; sickle cell crisis;  
 KW urinary tract infection; progressive respiratory failure; septicemia;  
 KW ischemia; arthritis; asthma; cerebritis; bronchitis; vasculitis.  
 XX Homo sapiens.  
 OS  
 XX WO200109616-A2.  
 XX  
 XX 08-FEB-2001.  
 XX  
 XX 02-AUG-2000; 2000WO-US21101.  
 XX  
 XX 02-AUG-1999; 99US-0146680.  
 XX  
 XX (UYDU-) UNIV DUKE.  
 XX (RERE-) RES & DEV INST INC.  
 XX  
 XX Stamler JS, Gow AJ, Singel DJ;  
 XX WPI; 2001-183002/18.  
 XX  
 XX Determining predominant physiological effect of composition comprising  
 PT hemoglobin used to produce methods of therapy for medical disorders by  
 PT using EPR or UV spectra of iron nitrosyl hemoglobin derivatives -  
 XX Disclosure; Fig 11; 70pp; English.  
 XX  
 XX This invention describes a novel method for determining the predominant

CC physiological effect of a composition comprising hemoglobin which  
 CC involves obtaining electron paramagnetic resonance (EPR) or UV spectra of  
 CC iron-nitrosyl hemoglobin derivatives formed by incubation of limiting  
 CC nitric oxide (NO) with hemoglobin and determining if the composition  
 CC shows non-cooperativity or cooperativity in binding of NO to the  
 CC hemoglobin. The products of the invention have antianemic; antibacterial;  
 CC immunosuppressive; vasotropic; antiinflammatory; antiasthmatic;  
 CC respiratory; antiarthritic and cerebroprotective activity. The products  
 CC of the invention are used to produce methods of therapy for medical  
 CC disorders characterized by red blood cell membrane defects and for a  
 CC variety of hypercoagulable and vasculopathic states, particularly for  
 CC patients with septic shock who develop myocardial depression,  
 CC pancreatitis and progressive respiratory failure, patients with  
 CC septicemia as a complication of urinary tract infection and patients with  
 CC ischemia, patients in a sickle cell crisis and for treating inflammatory  
 CC conditions such as arthritis, asthma, cerebritis, bronchitis and  
 CC vasculitis. The methods are also used for preserving red blood cells  
 CC which can be used in therapy.

XX SQ Sequence 911 AA;

Query Match 100.0%; Score 96; DB 22; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAAIQIEVKEQRI 20  
 |||||  
 Db 742 GKASTPGAAAIQIEVKEQRI 761

#### RESULT 13

AAE29343  
 ID AAE29343 standard; Protein; 911 AA.

XX  
 AC AAE29343;

XX 27-JAN-2003 (first entry)

XX Human Band 3 protein #1.

XX Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
 KW protozoacide; gene therapy.

XX Homo sapiens.

XX WO200270542-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002WO-US06415.

XX 02-MAR-2001; 2001US-272930P.

XX (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX Chishtl AH, Oh SS, Liu D, Goel V;

XX WPI; 2002-759814/82.

XX N-PSDB; AAD46978.

PT New isolated Band 3 polypeptide which selectively binds to merozoite  
 PT surface protein-1, useful for the prevention and treatment of malarial  
 PT infection

PS Disclosure; Page 102-105; 163pp; English.

XX The invention relates to an isolated Band 3 polypeptide that comprises  
 CC any of 4 20 residue amino acid sequences, or their fragments that bind  
 CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
 CC pair sequences. The methods and compositions of the present invention  
 CC are useful for the prevention and treatment of malarial infection. The  
 CC present invention, develops new and more improved methods based upon  
 CC inhibiting the particular interactions between the malarial parasite and

CC a cognate molecule present in the host and subsequently minimising  
 CC harmful side effects and drug resistance that may be due to non-specific  
 CC therapeutic approaches. The invention is useful in gene therapy. The  
 CC present invention also provides a vaccine for malaria. The present  
 CC sequence is human Band 3 protein.

XX SQ Sequence 911 AA;

Query Match 100.0%; Score 96; DB 23; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAAIQIEVKEQRI 20  
 |||||  
 Db 742 GKASTPGAAAIQIEVKEQRI 761

#### RESULT 14

AAE29344  
 ID AAE29344 standard; Protein; 911 AA.

XX  
 AC AAE29344;

XX 27-JAN-2003 (first entry)

XX Human Band 3 protein #2.

XX Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
 KW protozoacide; gene therapy.

XX Homo sapiens.

XX WO200270542-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002WO-US06415.

XX 02-MAR-2001; 2001US-272930P.

XX (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX Chishtl AH, Oh SS, Liu D, Goel V;

XX WPI; 2002-759814/82.

XX N-PSDB; AAD46979.

PT New isolated Band 3 polypeptide which selectively binds to merozoite  
 PT surface protein-1, useful for the prevention and treatment of malarial  
 PT infection

PS Disclosure; Page 107-110; 163pp; English.

XX The invention relates to an isolated Band 3 polypeptide that comprises  
 CC any of 4 20 residue amino acid sequences, or their fragments that bind  
 CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
 CC pair sequences. The methods and compositions of the present invention  
 CC are useful for the prevention and treatment of malarial infection. The  
 CC present invention, develops new and more improved methods based upon  
 CC inhibiting the particular interactions between the malarial parasite and  
 CC a cognate molecule present in the host and subsequently minimising  
 CC harmful side effects and drug resistance that may be due to non-specific  
 CC therapeutic approaches. The invention is useful in gene therapy. The  
 CC present invention also provides a vaccine for malaria. The present  
 CC sequence is human Band 3 protein.

XX SQ Sequence 911 AA;

Query Match 100.0%; Score 96; DB 23; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAAIQIEVKEQRI 20

Db 742 GKASTPGAAQIOEVKEQRI 761  
|||||

## RESULT 15

AAU30825  
ID AAU30825 standard; Protein; 962 AA.

XX AC AAU30825;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #1316.

XX KW Human; vaccination; gene therapy; nutritional supplement;

XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US08656.

XX PR 18-APR-2000; 2000US-0552929.

XX PR 26-JAN-2001; 2001US-0770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic

XX PS vaccination, testing and therapy -

XX CC Claim 20; Page 354; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The

XX CC polypeptides and antibodies to the polypeptides are useful for

XX CC determining the presence of or predisposition to a disease associated

XX CC with altered levels of polypeptide. The polypeptides are also useful for

XX CC identifying agents (agonists and antagonists) that bind to them. Cells

XX CC expressing the proteins are useful for identifying a therapeutic agent

XX CC for use in treatment of a pathology related to aberrant expression or

XX CC physiological interactions of the polypeptide. Vectors comprising

XX CC the nucleic acids encoding the polypeptides and cells genetically

XX CC engineered to express them are also useful for producing the proteins.

XX CC The proteins are useful in genetic vaccination, testing and

XX CC therapy, and can be used as nutritional supplements. They may be used to

XX CC increase stem cell proliferation; to regulate haematopoiesis; and in

XX CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;

XX CC immune suppression and/or stimulation; as anti-inflammatory agents; and

XX CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid

XX CC sequences of novel human secreted proteins of the invention.

XX SQ Sequence 962 AA;

Query Match 100.0%; Score 96; DB 22; Length 962;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAQIOEVKEQRI 20

DB 793 GKASTPGAAQIOEVKEQRI 812

|||||

Search completed: September 3, 2003, 11:46:12

Job time : 49.5 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:24:37 ; Search time 48.5 Seconds  
(without alignments)  
65.454 Million cell updates/sec

Title: US-10-087-464-4

Perfect score: 112

Sequence: 1 DRILLFKPKYHPDVPYK 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	100.0	20	AAE29342	Human Band 3 pepti
2	112	100.0	51	AAE29350	Human Band 3 prote
3	112	100.0	58	AAW01095	Exofacial region 1
4	112	100.0	58	AAE74886	Human band 3 prote
5	112	100.0	911	AAE15355	Human erythrocyte
6	112	100.0	911	AAW90263	A. tigrinum AEL pr
7	112	100.0	911	AAE46914	Human erythrocyte
8	112	100.0	911	AAE29343	Human Band 3 prote
9	112	100.0	911	AAE29344	Human Band 3 prote

10	112	100.0	962	22	AAU30825	Novel human secret
11	89	79.5	16	18	AAW18594	Aged band 3 peptid
12	89	79.5	19	18	AAW18595	Aged band 3 peptid
13	79	70.5	14	17	AAW01080	Anion transporter
14	79	70.5	14	22	AAE74852	Band 3 protein loo
15	74	66.1	1240	20	AAW90262	A. tigrinum AE2 pr
16	68	60.7	1030	20	AAW90261	A. tigrinum AE3 pr
17	66	58.9	292	7	AAE60645	Mouse kidney cell
18	63	56.2	1035	20	AAW90260	A. tigrinum NBC pr
19	62	55.4	56	22	ABE48986	Human liver peptid
20	62	55.4	56	22	ABB28984	Peptide #1635 enco
21	62	55.4	56	22	ABB34152	Peptide #1638 enco
22	62	55.4	56	22	ABE19596	Protein #1595 enco
23	62	55.4	56	22	AAE54944	Human brain expres
24	62	55.4	56	22	AAE67324	Human bone marrow
25	62	55.4	56	22	AAE15159	Peptide #1593 enco
26	62	55.4	56	22	AAE27616	Peptide #1633 enco
27	62	55.4	56	22	AAE02897	Peptide #1579 enco
28	62	55.4	56	23	ABG36967	Human peptide enco
29	62	55.4	773	21	ABG23336	Drosophila Na+ dri
30	62	55.4	774	21	ABG23340	Drosophila Na+ dri
31	62	55.4	779	21	ABG23341	Drosophila Na+ dri
32	62	55.4	779	21	ABG23342	Drosophila Na+ dri
33	62	55.4	1017	22	ABE60785	Drosophila melanog
34	62	55.4	1030	21	ABE23337	Drosophila Na+ dri
35	62	55.4	1086	22	ABE60786	Drosophila melanog
36	62	55.4	1086	23	ABG70008	Larval viability a
37	61	54.5	1030	21	ABE23339	Drosophila Na+ dri
38	58	51.8	227	22	AAE00872	Human bone marrow
39	58	51.8	348	22	AAE00759	Human bone marrow
40	58	51.8	440	23	ABE69662	Human polypeptide
41	58	51.8	440	23	ABE79586	Human suppressor o
42	58	51.8	440	23	ABE60995	Novel human protei
43	58	51.8	440	24	ABE55448	Human suppressor o
44	55	49.1	10	18	AAW18606	Aged band 3 peptid
45	52	46.4	314	23	AAE48755	Human adipose tiss

## ALIGNMENTS

### RESULT 1

AAE29342  
ID AAE29342 standard; peptide; 20 AA.

XX AAE29342;

AC AAE29342;

XX 27-JAN-2003 (first entry)

DT Human Band 3 peptide, B36A.

DE Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;

DE protozoacide; gene therapy.

KW Homo sapiens.

XX WO200270542-A2.

PN 12-SEP-2002.

PD 01-MAR-2002; 2002WO-US06415.

PF 02-MAR-2001; 2001US-272930P.

XX (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX Chisht AH, Oh SS, Liu D, Goel V;

XX WPI; 2002-759814/82.

XX New isolated Band 3 polypeptide which selectively binds to merozoite

XX surface protein-1, useful for the prevention and treatment of malarial

XX infection

XX Claim 1; Page 84; 163pp; English.

XX The invention relates to an isolated Band 3 polypeptide that comprises

CC any of 4 20 residue amino acid sequences, or their fragments that bind

CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base

CC pair sequences. The methods and compositions of the present invention

CC are useful for the prevention and treatment of malarial infection. The

CC present invention, develops new and more improved methods based upon

CC inhibiting the particular interactions between the malarial parasite and

CC a cognate molecule present in the host and subsequently minimising

CC harmful side effects and drug resistance that may be due to non-specific

CC therapeutic approaches. The invention is useful in gene therapy. The

CC present invention also provides a vaccine for malaria. The present

CC sequence is human Band 3 peptide.

XX Sequence 20 AA;

XX Query Match 100.0%; Score 112; DB 23; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 6.6e-10;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDVPYVK 20

Db 1 DRILLFKPKYHPDVPYVK 20

|||||

RESULT 2

AAE29350

ID AAE29350 standard; peptide; 51 AA.

XX AAE29350;

XX 27-JAN-2003 (first entry)

XX Human Band 3 protein ectoplasmic domain 6.

XX Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;

XX protozoacide; gene therapy.

XX Homo sapiens.

XX WO200270542-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002WO-US06415.

XX 02-MAR-2001; 2001US-272930P.

XX (SELI-) ST ELIZABETH'S MEDICAL CENT INC.

XX Chishti AH, Oh SS, Liu D, Goel V;

XX WPI; 2002-759814/82.

XX New isolated Band 3 polypeptide which selectively binds to merozoite

XX surface protein-1, useful for the prevention and treatment of malarial

XX infection

XX Example; Page 58; 163pp; English.

XX The invention relates to an isolated Band 3 polypeptide that comprises

CC any of 4 20 residue amino acid sequences, or their fragments that bind

CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base

CC pair sequences. The methods and compositions of the present invention

CC are useful for the prevention and treatment of malarial infection. The

CC present invention, develops new and more improved methods based upon

CC inhibiting the particular interactions between the malarial parasite and

CC a cognate molecule present in the host and subsequently minimising

CC harmful side effects and drug resistance that may be due to non-specific

CC therapeutic approaches. The invention is useful in gene therapy. The

CC present invention also provides a vaccine for malaria. The present

CC sequence is human Band 3 protein ectoplasmic domain 6.

XX Sequence 51 AA;

XX Query Match 100.0%; Score 112; DB 23; Length 51;

XX Best Local Similarity 100.0%; Pred. No. 1.8e-09;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDVPYVK 20

Db 1 DRILLFKPKYHPDVPYVK 20

|||||

RESULT 3

AAW01095

ID AAW01095 standard; peptide; 58 AA.

XX AAW01095;

XX 08-MAY-1997 (first entry)

XX Exofacial region loop 7 of band 3 protein (residues 800-857).

XX Anion transporter band 3 protein; endothelial adhesion; red blood cell;

XX cytoplasmic domain; erythrocyte; exofacial loop; epitope; antibody;

XX mammal; plasmodium falciparum infection; sickle cell disease; diabetes;

XX band 3; thalassaemia; anaemia; therapy.

XX Synthetic.

XX WO9629086-A1.

XX 26-SEP-1996.

XX 07-MAR-1996; 96WO-US03180.

XX 17-MAR-1995; 95US-0405647.

XX (REGC ) UNIV CALIFORNIA.

XX Crandall IE, Sherman IW, Shohet SB, Thevenin BJ;

XX WPI; 1996-442944/44.

XX Peptide(s) with amino acid motifs in band 3 - used for reducing the

XX adhesiveness of red blood cells for treating malaria, sickle cell

XX disease, thalassemia or diabetes.

XX Example 2; Page 20; 48pp; English.

XX AAW01053-W01095 represent peptides isolated from (or based on) regions

XX of the anion transporter band 3 protein. The band 3 protein is present

XX in a million copies per red blood cell, in the form of monomers, dimers,

XX or tetramers. Band 3 protein has two distinct domains, a 43 kD

XX water-soluble cytoplasmic domain, and a 55 kD membrane spanning domain.

XX In an number of otherwise-unrelated conditions (such as malaria, and

XX diabetes), there are modifications in band 3, such that there is

XX clustering and a change in the conformation of the protein. Due to this

XX change in protein conformation (and by the exposure of cryptic adhesive

XX sites), the normally non-adherent erythrocyte becomes a cell with the

XX enhanced endothelial adhesiveness. These sequences were found in the

XX putative exofacial loops of band 3, and are epitopes for antibody

XX binding. These sequences compete with the altered band 3 protein, and

XX thereby block the adhesiveness of the red blood cells. The peptides can

XX be used for reducing the adhesiveness of red blood cells in a mammalian

XX patient characterised by a condition selected from plasmodium falciparum

XX infection, sickle cell disease, thalassaemia and diabetes.

XX Sequence 58 AA;

XX Query Match 100.0%; Score 112; DB 17; Length 58;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-09;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDPVPVK 20  
 |||||  
 Db 8 DRILLFKPKYHPDPVPVK 27

RESULT 4  
 AAB74886  
 ID AAB74886 standard; peptide; 58 AA.

XX AC AAB74886;

XX DT 19-JUN-2001 (first entry)

XX DE Human band 3 protein predicted exofacial region loop 7 SEQ ID NO:43.

XX KW Anti-Plasmodium falciparum; interaction inhibitor; band 3 protein;  
 KW thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarction;  
 KW lysis; ventricular function; congestive heart failure; mortality;  
 KW acute arterial thrombosis; embolism; thrombosis; cerebral sinus.

XX OS Homo sapiens.

XX PN US6191103-B1.

XX PD 20-FEB-2001.

XX PF 05-DEC-1997; 97US-0985499.

XX PR 05-DEC-1997; 97US-0985499.

XX PA (REGC ) UNIV CALIFORNIA.

XX PB (BLOO-) CENT BLOOD RES.

PI Shohet SB, Sherman I, Von Andrian U;

XX WPI; 2001-307101/32.

XX Enhancing thrombolysis in mammals comprises administering an inhibitor  
 of protein band 3-ligand interaction

PS Disclosure; Column 7; 23pp; English.

XX The present invention describes a method for enhancing thrombolysis in  
 CC a mammal. The method comprises the administration to the mammal an  
 CC amount of an inhibitor (I) of protein band 3-ligand interaction  
 CC sufficient to enhance thrombolysis. (I) has thrombolytic activity.  
 CC The method is useful for enhancing thrombolysis in a mammal. (I) is  
 CC useful for enhancing fibrinolytic or thrombolytic activity, in the  
 CC management of acute myocardial infarction, for lysis of intracoronary  
 CC thrombi, for improvement of ventricular function, for reduction of  
 CC congestive heart failure, for reduction of mortality, for the lysis of  
 CC pulmonary emboli blocking blood flow to one or more lobes of the lung,  
 CC for the lysis of acute arterial thrombosis and embolism, for the lysis  
 CC of thrombosis in deep veins or in cerebral sinuses, to reopen i.v.  
 CC catheters obstructed by clotted blood or fibrin, to prevent clot  
 CC formation of lysing clots, to prevent clotting in blood samples drawn  
 CC from patients for clinical testing and to prevent the recurrence of  
 CC thrombosis in patients by prophylactic administration. The present  
 CC sequence represents a human band 3 protein predicted exofacial region  
 CC loop peptide, which is used in the exemplification of the present  
 CC invention.

XX Sequence 58 AA;

Query Match 100.0%; Score 112; DB 22; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2.le-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDPVPVK 20  
 |||||  
 Db 8 DRILLFKPKYHPDPVPVK 27

RESULT 5  
 AAR15355  
 ID AAR15355 standard; Protein; 911 AA.

XX AC AAR15355;

XX DT 25-MAR-2003 (updated)

XX DT 08-MAR-1992 (first entry)

XX DE Human erythrocyte membrane anion-transport protein (band 3).

XX KW Senescent cell peptide; ANION 1; COOH; auto immune disease.

XX OS Homo sapiens.

XX PN WO9118013-A.

XX PD 28-NOV-1991.

XX PF 24-MAY-1991; 91WO-US03557.

XX PR 24-MAY-1990; 90US-0528210.

XX PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.

XX PI Kay MBM, Marchalonis JJ;

XX DR WPI; 1991-369184/50.

XX DR N-PSDB; AAQ15172.

XX Synthetic senescent cell antigen and peptide(s) - used to detect  
 PT antibodies to SCA, study cellular ageing and auto-immune  
 PT mechanisms, separate anions and treat auto-immune disease

XX PS Disclosure; Fig 1; 74pp; English.

XX The amino acid sequence is that of the human erythrocyte anion-transport  
 CC protein (band 3). Amino acids 538-554 (ANION 1) or 812-827 (COOH) code  
 CC for a peptide which is immuno-reactive with antibodies to senescent cell  
 CC antigen (SCA). The antigen and peptides can be used in any method or  
 CC technique involving or requiring the inhibition of the binding of  
 CC senescent cell IgG to senescent cells in vitro or in vivo. The prods.  
 CC can be used in to examine various physiological, biochemical, and  
 CC immunological mechanisms in humans and other animals, such as those  
 CC relating to cellular ageing, degeneration, and life span; removal of  
 CC senescent cells; anion transport across cellular membranes; disease  
 CC mechanisms where increased senescent cell IgG may play a role, such  
 CC as haemolytic anaemia, sickle cell anaemia, and idiopathic  
 CC thrombocytopenia purpura; other autoimmune disease mechanisms, such  
 CC as rheumatoid arthritis and systemic lupus erythematosus; and other  
 CC diseases such as those involved in malaria and cancer. More  
 CC specifically, the prods. are useful in cosmetic and pharmaceutical  
 CC compsns., diagnostic kits, and methods for detecting or measuring  
 CC Abs to SCA, studying cellular ageing and autoimmune mechanisms,  
 CC separating anions from a gas or liquid, or diagnosis and treatment  
 CC of certain diseases.  
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 911 AA;

Query Match 100.0%; Score 112; DB 12; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDPVPVK 20  
 |||||  
 Db 807 DRILLFKPKYHPDPVPVK 826

RESULT 6  
 AAW90263  
 ID AAW90263 standard; peptide; 911 AA.



KW Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
 KW protozoacide; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200270542-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 01-MAR-2002; 2002WO-US06415.  
 XX  
 PR 02-MAR-2001; 2001US-272930P.  
 XX  
 PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.  
 XX  
 PI Chishtli AH, Oh SS, Liu D, Goel V;  
 XX  
 DR WPI: 2002-759814/82.  
 DR N-PSDB; AAD46978.  
 XX  
 PT New isolated Band 3 polypeptide which selectively binds to merozoite  
 PT surface protein-1, useful for the prevention and treatment of malarial  
 PT infection -  
 XX  
 PS Disclosure; Page 102-105; 163pp; English.  
 XX  
 CC The invention relates to an isolated Band 3 polypeptide that comprises  
 CC any of 4 20 residue amino acid sequences, or their fragments that bind  
 CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
 CC pair sequences. The methods and compositions of the present invention  
 CC are useful for the prevention and treatment of malarial infection. The  
 CC present invention, develops new and more improved methods based upon  
 CC inhibiting the particular interactions between the malarial parasite and  
 CC a cognate molecule present in the host and subsequently minimising  
 CC harmful side effects and drug resistance that may be due to non-specific  
 CC therapeutic approaches. The invention is useful in gene therapy. The  
 CC present invention also provides a vaccine for malaria. The present  
 CC sequence is human Band 3 protein.  
 XX  
 SQ Sequence 911 AA;  
 Query Match 100.0%; Score 112; DB 23; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DRILLFKPKYHPDVPYVK 20  
 ||||||||||||||||  
 DB 807 DRILLFKPKYHPDVPYVK 826  
 RESULT 9  
 AA29344  
 ID AAE29344 standard; Protein; 911 AA.  
 XX  
 AC AAE29344;  
 XX  
 DT 27-JAN-2003 (first entry)  
 XX  
 DE Human Band 3 protein #2.  
 XX  
 KW Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;  
 KW protozoacide; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200270542-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 01-MAR-2002; 2002WO-US06415.  
 XX  
 PR 02-MAR-2001; 2001US-272930P.  
 XX

PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.  
 XX  
 PI Chishtli AH, Oh SS, Liu D, Goel V;  
 XX  
 DR WPI: 2002-759814/82.  
 DR N-PSDB; AAD46979.  
 XX  
 PT New isolated Band 3 polypeptide which selectively binds to merozoite  
 PT surface protein-1, useful for the prevention and treatment of malarial  
 PT infection -  
 XX  
 PS Disclosure; Page 107-110; 163pp; English.  
 XX  
 CC The invention relates to an isolated Band 3 polypeptide that comprises  
 CC any of 4 20 residue amino acid sequences, or their fragments that bind  
 CC to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base  
 CC pair sequences. The methods and compositions of the present invention  
 CC are useful for the prevention and treatment of malarial infection. The  
 CC present invention, develops new and more improved methods based upon  
 CC inhibiting the particular interactions between the malarial parasite and  
 CC a cognate molecule present in the host and subsequently minimising  
 CC harmful side effects and drug resistance that may be due to non-specific  
 CC therapeutic approaches. The invention is useful in gene therapy. The  
 CC present invention also provides a vaccine for malaria. The present  
 CC sequence is human Band 3 protein.  
 XX  
 SQ Sequence 911 AA;  
 Query Match 100.0%; Score 112; DB 23; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DRILLFKPKYHPDVPYVK 20  
 ||||||||||||||||  
 DB 807 DRILLFKPKYHPDVPYVK 826  
 RESULT 10  
 AAU30825  
 ID AAU30825 standard; Protein; 962 AA.  
 XX  
 AC AAU30825;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Novel human secreted protein #1316.  
 XX  
 KW Human; vaccination; gene therapy; nutritional supplement;  
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200179449-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 16-APR-2001; 2001WO-US08656.  
 XX  
 PR 18-APR-2000; 2000US-0552929.  
 PR 26-JAN-2001; 2001US-0770160.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI: 2001-611725/70.  
 XX  
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic  
 PT vaccination, testing and therapy -  
 XX  
 PS Claim 20; Page 354; 765pp; English.  
 XX

CC The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent or  
 CC for use in treatment of a pathology related to aberrant expression or  
 CC physiological interactions of the polypeptide. Vectors comprising  
 CC the nucleic acids encoding the polypeptides and cells genetically  
 CC engineered to express them are also useful for producing the proteins.  
 CC The proteins are useful in genetic vaccination, testing and  
 CC therapy, and can be used as nutritional supplements. They may be used to  
 CC increase stem cell proliferation; to regulate haematopoiesis; and in  
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;  
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and  
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid  
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 962 AA;

Query Match 100.0%; Score 112; DB 22; Length 962;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDVPYVK 20  
 |||||  
 Db 858 DRILLFKPKYHPDVPYVK 877

#### RESULT 11

AAW18594  
 ID AAW18594 standard; peptide; 16 AA.

XX AAW18594;

DT 04-MAR-1998 (first entry)

XX Aged band 3 peptide (residues 812-827) epitope I.

XX Band 3 protein; antibody; aging antigenic site; Alzheimer's disease;  
 KW phosphorylation; detection; epitope.

XX Homo sapiens.

XX WO9726537-A1.

XX 24-JUL-1997.

XX 13-DEC-1996; 96WO-US20465.

XX 19-JAN-1996; 96US-0010250.

XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.

XX Key MMB;

XX WPI; 1997-385478/35.

XX Detecting Alzheimer's disease using antibody that recognises aged  
 PT band 3 protein in tissues - or from reduced degree of band 3 protein  
 PT phosphorylation, can be applied to blood or brain samples

XX Claim 6; Page 11; 45pp; English.

XX This is an aging antigenic band 3 peptide (residues 812-827) to which a  
 CC specific antibody can bind to. Band 3 is a ubiquitous anion-exchange  
 CC protein and ages as cells and tissues age. Antibodies have been developed  
 CC against this aged band 3. These antibodies bind to distinct regions of  
 CC band 3 in old cells (aging antigenic sites) but not middle aged or young  
 CC cells. This can be used for detecting Alzheimer's disease. A tissue  
 CC sample containing band 3 from a patient suspected of having Alzheimer's  
 CC disease is treated with an antibody that can differentiate between the  
 CC Alzheimer's (aged) and normal band 3, under complex-forming conditions

CC and detecting any complex formed. A tissue containing band 3 from a  
 CC healthy control is treated in a similar manner and the amounts of complex  
 CC formed are compared. A significantly greater formation of complex in the  
 CC suspect sample as compared with that of the control is indicative of  
 CC Alzheimer's disease. The disease can also be detected by comparing the  
 CC degrees of phosphorylation of band 3 or its degradation products in  
 CC suspect and control samples. A significant decrease in phosphorylation  
 CC in the suspect sample indicates Alzheimer's disease.

XX Sequence 16 AA;

Query Match 79.5%; Score 89; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LFKPPKYHPDVPYVK 20  
 |||||  
 Db 1 LFKPPKYHPDVPYVK 15

#### RESULT 12

AAW18595  
 ID AAW18595 standard; peptide; 19 AA.

XX AAW18595;

DT 04-MAR-1998 (first entry)

XX Aged band 3 peptide (residues 812-830) epitope II.

XX Band 3 protein; antibody; aging antigenic site; Alzheimer's disease;  
 KW phosphorylation; detection; epitope.

XX Homo sapiens.

XX WO9726537-A1.

XX 24-JUL-1997.

XX 13-DEC-1996; 96WO-US20465.

XX 19-JAN-1996; 96US-0010250.

XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.

XX Key MMB;

XX WPI; 1997-385478/35.

XX Detecting Alzheimer's disease using antibody that recognises aged  
 PT band 3 protein in tissues - or from reduced degree of band 3 protein  
 PT phosphorylation, can be applied to blood or brain samples

XX Claim 7; Page 10; 45pp; English.

XX This is an aging antigenic band 3 peptide (residues 812-830) to which a  
 CC specific antibody can bind to. Band 3 is a ubiquitous anion-exchange  
 CC protein and ages as cells and tissues age. Antibodies have been developed  
 CC against this aged band 3. These antibodies bind to distinct regions of  
 CC band 3 in old cells (aging antigenic sites) but not middle aged or young  
 CC cells. This can be used for detecting Alzheimer's disease. A tissue  
 CC sample containing band 3 from a patient suspected of having Alzheimer's  
 CC disease is treated with an antibody that can differentiate between the  
 CC Alzheimer's (aged) and normal band 3, under complex-forming conditions  
 CC and detecting any complex formed. A tissue containing band 3 from a  
 CC healthy control is treated in a similar manner and the amounts of complex  
 CC formed are compared. A significantly greater formation of complex in the  
 CC suspect sample as compared with that of the control is indicative of  
 CC Alzheimer's disease. The disease can also be detected by comparing the  
 CC degrees of phosphorylation of band 3 or its degradation products in  
 CC suspect and control samples. A significant decrease in phosphorylation  
 CC in the suspect sample indicates Alzheimer's disease.

XX

SQ Sequence 19 AA;

Query Match 79.5%; Score 89; DB 18; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LFKPKYHPDVPYVK 20  
 |||||  
 DB 1 LFKPKYHPDVPYVK 15

RESULT 13

AAW01080  
 ID AAW01080 standard; peptide; 14 AA.

XX AAW01080;

DT 08-MAY-1997 (first entry)

XX Anion transporter band 3 protein residues 814-827.

XX Anion transporter band 3 protein; endothelial adhesion; red blood cell;  
 KW cytoplasmic domain; erythrocyte; exofacial loop; epitope; antibody;  
 KW mammal; plasmodium falciparum infection; sickle cell disease; diabetes;  
 KW band 3; thalassaemia; anaemia; therapy.

XX Synthetic.

XX WO9629086-A1.

XX 26-SEP-1996.

PF 07-MAR-1996; 96WO-US03180.

PR 17-MAR-1995; 95US-0405647.

XX (REGC ) UNIV CALIFORNIA.

PI Crandall IE, Sherman IW, Shohet SB, Thevenin BJ;

DR WPI; 1996-442944/44.

XX Peptide(s) with amino acid motifs in band 3 - used for reducing the  
 PT adhesiveness of red blood cells for treating malaria, sickle cell  
 PT disease, thalassaemia or diabetes.

PS Disclosure; Page 12; 48pp; English.

XX AAW01053-W01095 represent peptides isolated from (or based on) regions  
 CC of the anion transporter band 3 protein. The band 3 protein is present  
 CC in a million copies per red blood cell, in the form of monomers, dimers,  
 CC or tetramers. Band 3 protein has two distinct domains, a 43 kD  
 CC water-soluble cytoplasmic domain, and a 55 kD membrane spanning domain.  
 CC In an number of otherwise-unrelated conditions (such as malaria, and  
 CC diabetes), there are modifications in band 3, such that there is  
 CC clustering and a change in the conformation of the protein. Due to this  
 CC change in protein conformation (and by the exposure of cryptic adhesive  
 CC sites), the normally non-adherent erythrocyte becomes a cell with  
 CC enhanced endothelial adhesiveness. These sequences were found in the  
 CC putative exofacial loops of band 3, and are epitopes for antibody  
 CC binding. These sequences compete with the altered band 3 protein, and  
 CC thereby block the adhesiveness of the red blood cells. The peptides can  
 CC be used for reducing the adhesiveness of red blood cells in a mammalian  
 CC patient characterised by a condition selected from Plasmodium falciparum  
 CC infection, sickle cell disease, thalassaemia and diabetes.

SQ Sequence 14 AA;

Query Match 70.5%; Score 79; DB 17; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPPKYHPDVPYVK 20

DB 1 KPPKYHPDVPYVK 13  
 |||||

RESULT 14

AAW74852  
 ID AAW74852 standard; peptide; 14 AA.

XX AAW74852;

DT 19-JUN-2001 (first entry)

XX Band 3 protein loop 3 related peptide SEQ ID NO:9.

XX Anti-Plasmodium falciparum; interaction inhibitor; band 3 protein;  
 KW thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarction;  
 KW lysis; ventricular function; congestive heart failure; mortality;  
 KW acute arterial thrombosis; embolism; thrombosis; cerebral sinus.

XX Synthetic.

XX US6191103-B1.

XX 20-FEB-2001.

PF 05-DEC-1997; 97US-0985499.

PR 05-DEC-1997; 97US-0985499.

PA (REGC ) UNIV CALIFORNIA.

XX (BLOO-) CENT BLOOD RES.

XX Shohet SB, Sherman I, Von Andrian U;

DR WPI; 2001-307101/32.

XX Enhancing thrombolysis in mammals comprises administering an inhibitor  
 PT of protein band 3-ligand interaction

PS Disclosure; Column 8; 23pp; English.

XX The present invention describes a method for enhancing thrombolysis in  
 CC a mammal. The method comprises the administration to the mammal an  
 CC amount of an inhibitor (I) of protein band 3-ligand interaction  
 CC sufficient to enhance thrombolysis. (I) has thrombolytic activity.  
 CC The method is useful for enhancing thrombolysis in a mammal. (I) is  
 CC useful for enhancing fibrinolytic or thrombolytic activity, in the  
 CC management of acute myocardial infarction, for lysis of intracoronary  
 CC thrombi, for improvement of ventricular function, for reduction of  
 CC congestive heart failure, for reduction of mortality, for the lysis of  
 CC pulmonary emboli blocking blood flow to one or more lobes of the lung,  
 CC for the lysis of acute arterial thrombosis and embolism, for the lysis  
 CC of thrombosis in deep veins or in cerebral sinuses, to reopen i.v.  
 CC catheters obstructed by clotted blood or fibrin, to prevent clot  
 CC formation of lysing clots, to prevent clotting in blood samples drawn  
 CC from patients for clinical testing and to prevent the recurrence of  
 CC thrombosis in patients by prophylactic administration. The present  
 CC sequence represents a band 3 protein loop 3 related peptide, which  
 CC is given in the exemplification of the present invention.

SQ Sequence 14 AA;

Query Match 70.5%; Score 79; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPPKYHPDVPYVK 20

DB 1 KPPKYHPDVPYVK 13

RESULT 15

AAW90262

ID	AAW90262	standard; peptide; 1240 AA.
XX	AAW90262;	
XX	27-APR-1999	(first entry)
XX	A. tigrinum	AE2 protein.
XX	NBC;	sodium bicarbonate transporter family; pH regulation; immunoassay;
XX	treatment;	water retention; blood pressure; acidosis; inflammation;
XX	cell proliferation;	cancer; sperm activation; inactivation; epilepsy;
XX	hydroencephaly;	glaucoma; colitis; salamander; AE2; anion exchange.
OS	Ambystoma	tigrinum.
XX	WO9853067-A1.	
XX	26-NOV-1998.	
XX	20-MAY-1998;	98WO-US10297.
XX	20-MAY-1997;	97US-0047131.
XX	{UYUA }	UNIV YALE.
XX	Aalkjaer C,	Bevensee MO, Biemesderfer D, Boron WF;
XX	Choi I, Davis BA,	Grichtchenko II, Romero MF, Schmitt BM;
XX	Sussman CR;	
XX	WPI;	1999-059743/05.
XX	New nucleic acid molecules	encoding proteins of the Sodium
XX	Bicarbonate Cotransporter (NBC)	family - useful for identifying
XX	agents that agonise or antagonise	NBC activity and treating
XX	disorders mediated by NBC	
XX	Example 1;	Fig 5; 138pp; English.
XX	This sequence represents	the anion exchange protein AE2 which is used in
XX	a method resulting in	the isolation of a novel salamander sodium
XX	bicarbonate transporter (NBC).	NBC proteins and nucleic acid sequences
XX	may be used to treat	pathological processes including water retention,
XX	increased blood pressure,	chronic respiratory and metabolic acidosis,
XX	inflammation, cell proliferation,	cancer, sperm activation/inactivation,
XX	hydroencephaly, epilepsy,	glaucoma and colitis. Members of the NBC family
XX	of proteins can be used	(i) as a target to identify agents that block or
XX	stimulate NBC mediated	pH regulation, (ii) as a target or bait to
XX	identify and isolate	binding partners that bind NBC, (iii) in methods to
XX	identify agents that	block or stimulate activity of an NBC protein, and
XX	(iv) as a target to	assay for NBC-mediated activity. Anti-NBC antibodies
XX	are also useful as	modulators of NBC activity, useful in the immunoassays
XX	for detecting NBC	expression/activity and for purifying an NBC protein.
XX	Sequence	1240 AA;
XX	Query Match	56.1%; Score 74; DB 20; Length 1240;
XX	Best Local Similarity	65.0%; Pred. No. 0.026;
XX	Matches 13; Conservative	3; Mismatches 4; Indels 0; Gaps 0;
QY	1	DRILLFKPKYHPDVPYVK 20
DB	1136	ERLHLLMLPPKHHPDVTYVK 1155
		:-:       :

Search completed: September 3, 2003, 11:46:13  
Job time : 49.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:25:42 ; Search time 9.25 Seconds  
(without alignments)  
101.679 Million cell updates/sec

Title: US-10-087-464-1

Perfect score: 104

Sequence: 1 GMPWLSATTVRSYTHANALT 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	104	100.0	911	1	B3AT_HUMAN	P02730	homo sapien
2	104	100.0	927	1	B3AT_RAT	P23562	rattus norv
3	104	100.0	929	1	B3AT_MOUSE	P04919	mus musculus
4	100	96.2	922	1	B3AT_CHICK	P15575	gallus gall
5	95	91.3	918	1	B3AT_ONCMV	P32847	oncorhynch
6	93	89.4	1234	1	B3A2_RAT	P23347	rattus norv
7	93	89.4	1237	1	B3A2_MOUSE	P13808	mus musculus
8	93	89.4	1237	1	B3A2_RABIT	P48746	oryctolagus
9	89	85.6	1241	1	B3A2_HUMAN	P04920	homo sapien
10	89	85.6	1227	1	B3A3_MOUSE	P16283	mus musculus
11	89	85.6	1227	1	B3A3_RAT	P23348	rattus norv
12	89	85.6	1232	1	B3A3_HUMAN	P48751	homo sapien
13	89	85.6	1233	1	B3A3_RABIT	O18917	oryctolagus
14	83	79.8	1238	1	B3A2_CAVPO	Q92058	cavia porce
15	49	47.1	955	1	B3A4_RABIT	Q99KY1	oryctolagus
16	48	46.2	314	1	LIPA_MYCLE	O32962	mycobacteri
17	48	46.2	953	1	B3A4_RAT	O32962	mycobacteri
18	48	46.2	983	1	B3A4_HUMAN	Q96G91	homo sapien
19	45	43.3	302	1	COBK_METTH	O27083	methanobact
20	45	43.3	727	1	KGA_RAT	P51556	rattus norv
21	45	43.3	730	1	KGA_MOUSE	O88673	mus musculus
22	44	42.3	449	1	C13A_MYCTU	O08447	mycobacteri
23	44	42.3	891	1	SL11_HUMAN	Q8nbs3	homo sapien
24	43	41.3	115	1	N3JM_HYLLA	Q95708	hylobates l
25	43	41.3	311	1	LIPA_MYCTU	O10380	mycobacteri
26	43	41.3	431	1	UROK_HUMAN	P00749	homo sapien
27	43	41.3	1076	1	YKTS_SCHPO	Q9c104	schizosacch
28	42.5	40.9	552	1	NRFE_ECOLI	P32710	escherichia
29	42	40.4	354	1	PROW_ECOLI	P14176	escherichia
30	42	40.4	405	1	CYB_RHOU	P23134	rhodospiril
31	42	40.4	827	1	KGLL_CAEEL	Q03603	caenorhabdi
32	41	39.4	322	1	HEM3_CAUCR	Q9abz8	caulobacter
33	41	39.4	442	1	UROK_PIG	P04185	sus scrofa

## RESULT 1

B3AT\_HUMAN

ID B3AT\_HUMAN STANDARD; PRT; 911 AA.

AC P02730;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)

DE (CD233 antigen).

GN SLC4A1 OR AEL OR EPB3 OR DI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9008313; PubMed=2594752;

RA Lux S.E., John K.M., Kopito R.R., Lodish H.F.;

RT "Cloning and characterization of band 3, the human erythrocyte anion-

exchange protein (AE1).";

RL Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=89134172; PubMed=3223947;

RA Tanner M.J.A., Martin P.G., High S.;

RT "The complete amino acid sequence of the human erythrocyte membrane

anion-transport protein deduced from the cDNA sequence.";

RL Biochem. J. 256:703-712(1988).

RN [3]

RP SEQUENCE OF 1-199; 220-292 AND 347-370.

RX MEDLINE=90001294; PubMed=2790053;

RA Yannoukakos D., Vasseur C., Blouquit Y., Bursaux E., Wajzman H.;

RT "Primary structure of the cytoplasmic domain of human erythrocyte

protein band 3. Comparison with its sequence in the mouse.";

RL Biochim. Biophys. Acta 998:43-49(1989).

RN [4]

RP SEQUENCE OF 1-201.

RX MEDLINE=83238395; PubMed=6345535;

RA Kaul R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;

RT "Amino acid sequence of the N alpha-terminal 201 residues of human

erythrocyte membrane band 3.";

RL J. Biol. Chem. 258:7981-7990(1983).

RN [5]

RP SEQUENCE OF 1-3.

RX MEDLINE=79027186; PubMed=701248;

RA Drickamer L.K.;

RT "Orientation of the band 3 polypeptide from human erythrocyte

membranes. Identification of NH2-terminal sequence and site of

carbohydrate attachment.";

RL J. Biol. Chem. 253:7242-7248(1978).

RN [6]

RP SEQUENCE OF 559-630.

RX MEDLINE=83308584; PubMed=6615451;

RA Brock C.J., Tanner M.J.A., Kempf C.;

RT "The human erythrocyte anion-transport protein. Partial amino acid

sequence, conformation and a possible molecular mechanism for anion exchange.";  
 RL Biochem. J. 213:577-586(1983).  
 [7]  
 RN SEQUENCE OF 834-911.  
 RX MEDLINE-88228050; PubMed-3372523;  
 RA Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.;  
 RT "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein.";  
 RL J. Biol. Chem. 263:8232-8238(1988).  
 [8]  
 RN ROLE OF GLU-681, AND SEQUENCE OF 665-688.  
 RX MEDLINE-92332495; PubMed-1353774;  
 RA Jennings M.L., Smith J.S.;  
 RT "Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681.";  
 RL J. Biol. Chem. 267:13964-13971(1992).  
 [9]  
 RN PALMITOYLATION OF CYS-843.  
 RX MEDLINE-91358422; PubMed-1885574;  
 RA Okubo K., Hamasaki N., Hara K., Kageura M.;  
 RT "Palmitoylation of cysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICIAVL found in band 3 protein and G2 protein of Rift Valley fever virus.";  
 RL J. Biol. Chem. 266:16420-16424(1991).  
 [10]  
 RN PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.  
 RX MEDLINE-20400020; PubMed-10942405;  
 RA Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E., Pinna L.A., Donella-Deana A.;  
 RT "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites.";  
 RL Blood 96:1550-1557(2000).  
 [11]  
 RN VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-91329825; PubMed-1678289;  
 RA Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J., Wajcman H., Bursaux E.;  
 RT "Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the structural modification (Lys 56->Glu) by protein chemistry methods.";  
 RL Blood 78:1117-1120(1991).  
 [12]  
 RN VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-92107882; PubMed-1722314;  
 RA Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T., Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;  
 RT "Deletion in erythrocyte band 3 gene in malaria-resistant Southeast Asian ovalocytosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).  
 [13]  
 RN VARIANT HS ARG-327.  
 RX MEDLINE-92329950; PubMed-1378323;  
 RA Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C., Cohen C.M.;  
 RT "Band 3 fuscaloosa: Pro-327->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2.";  
 RL Blood 80:523-529(1992).  
 [14]  
 RN VARIANT HE 400-ALA--ALA-408 DEL.  
 RX MEDLINE-92167271; PubMed-1538403;  
 RA Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M., Nash G.B., Bluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M., Gratzel W.B.;  
 RT "Basis of unique red cell membrane properties in hereditary ovalocytosis.";  
 RL J. Mol. Biol. 223:949-958(1992).  
 [15]  
 RN VARIANT HS LEU-868.  
 RX MEDLINE-93343855; PubMed-8343110;

RA Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;  
 RT "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868->Leu in the membrane domain of band 3.";  
 RL Biochem. J. 293:317-320(1993).  
 [16]  
 RN VARIANT MONTEFIORE LYS-40.  
 RX MEDLINE-93229758; PubMed-8471774;  
 RA Rydicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L., Schwartz R.S.;  
 RT "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore).";  
 RL Blood 81:2155-2165(1993).  
 [17]  
 RN VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.  
 RX MEDLINE-94266802; PubMed-8206915;  
 RA Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;  
 RT "Band 3 Memphis variant II. Altered stilbene disulfonate binding and the Diego (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation Pro-854->Leu.";  
 RL J. Biol. Chem. 269:16155-16158(1994).  
 [18]  
 RN VARIANT BLOOD GROUP WR(A).  
 RX MEDLINE-95111140; PubMed-7812009;  
 RA Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S., Tanner M.J.;  
 RT "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain conditions.";  
 RL Blood 85:541-547(1995).  
 [19]  
 RN VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.  
 RX MEDLINE-95134893; PubMed-7530501;  
 RA Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S., Alper S.B., Brugnara C., Wichterle H., Palek J.;  
 RT "Mutations of conserved arginines in the membrane domain of erythrocyte band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis.";  
 RL Blood 85:634-640(1995).  
 [20]  
 RN VARIANT HS ASP-771.  
 RX MEDLINE-96136073; PubMed-8547122;  
 RA Maillet P., Vallier A., Reinhardt W.H., Wyss E.J., Ott P., Texier P., Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;  
 RT "Band 3 Chur: a variant associated with band 3-deficient hereditary spherocytosis and substitution in a highly conserved position of transmembrane segment 11.";  
 RL Br. J. Haematol. 91:804-810(1995).  
 [21]  
 RN VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.  
 RX MEDLINE-97099297; PubMed-8943874;  
 RA Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V., Palek J.;  
 RT "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency.";  
 RL Blood 88:4366-4374(1996).  
 [22]  
 RN VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.  
 RX MEDLINE-96225450; PubMed-8640229;  
 RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T., Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A., Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";  
 RL Nat. Genet. 13:214-218(1996).  
 [23]  
 RN VARIANTS HS SER-147 AND MET-488.  
 RX MEDLINE-97351102; PubMed-9207478;  
 RA Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon M., Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,

Query Match 100.0%; Score 104; DB 1; Length 911;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATVRSVTHANALT 20  
 |||||  
 DB 720 GMPWLSATVRSVTHANALT 739

RESULT 2  
 B3AT\_RAT  
 ID B3AT\_RAT STANDARD; PRT; 927 AA.  
 AC P23562;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1).  
 GN SLC4A1 OR AEL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE OF 46-927 FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=89255254; PubMed=2722777;  
 RA Kudrycki K.E., Shull G.E.;  
 RT "Primary structure of the rat kidney band 3 anion exchange protein  
 deduced from a cDNA.";  
 RL J. Biol. Chem. 264:8185-8192(1989).  
 RN [2]  
 RP SEQUENCE OF 1-45 FROM N.A.  
 RA Kudrycki K.E., Shull G.E.;  
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN  
 MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,  
 WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR  
 CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).  
 CC -!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 AND APPEARS TO BE TETRAMERIC.  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE  
 BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND  
 COLLECTING DUCTS.  
 CC -!- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms-2;  
 Name=Erythrocyte;  
 CC IsoId=P23562-1; Sequence=Displayed;  
 CC Name=Kidney;  
 CC IsoId=P23562-2; Sequence=VSP\_000455;  
 CC -!- TISSUE SPECIFICITY: Kidney.  
 CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; J04793; AAA40800.1; ALT\_INIT.  
 DR EMBL; J02943; AAA40801.1; -.  
 DR PIR; A33810; A33810.  
 DR HSSP; P02730; 1BPS.  
 DR InterPro; IPR001717; Anion\_exchanger.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;

Lipoprotein; Palmitate; Alternative splicing.  
 KW DOMAIN 1 420  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 421 927  
 FT TRANSMEM 421 927  
 FT TRANSMEM 441 473  
 FT TRANSMEM 454 473  
 FT TRANSMEM 477 496  
 FT TRANSMEM 508 527  
 FT TRANSMEM 540 558  
 FT TRANSMEM 559 585  
 FT TRANSMEM 585 604  
 FT TRANSMEM 605 619  
 FT TRANSMEM 620 640  
 FT TRANSMEM 641 676  
 FT TRANSMEM 677 696  
 FT TRANSMEM 715 735  
 FT TRANSMEM 779 796  
 FT TRANSMEM 801 822  
 FT TRANSMEM 860 881  
 FT CARBOHYD 658 858  
 FT LIPID 859 859  
 FT VARSPLIC 1 79  
 FT Missing (in isoform kidney).  
 FT /FTId=VSP\_000455.  
 SQ SEQUENCE 927 AA; 103172 MW; 681A228474E5E9DE CRC64;

Query Match 100.0%; Score 104; DB 1; Length 927;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATVRSVTHANALT 20  
 |||||  
 DB 736 GMPWLSATVRSVTHANALT 755

RESULT 3  
 B3AT\_MOUSE  
 ID B3AT\_MOUSE STANDARD; PRT; 929 AA.  
 AC P04919;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)  
 DE (MEB3).  
 GN SLC4A1 OR AEL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85268011; PubMed=2410791;  
 RA Kopito R.R., Lodish H.F.;  
 RT "Primary structure and transmembrane orientation of the murine anion  
 exchange protein.";  
 RL Nature 316:234-238(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86034211; PubMed=3840489;  
 RA Kopito R.R., Lodish H.F.;  
 RT "Structure of the murine anion exchange protein.";  
 RL J. Cell. Biochem. 29:1-17(1985).  
 RN [3]  
 RP PARTIAL SEQUENCE FROM N.A.  
 RX MEDLINE=87250387; PubMed=3036795;  
 RA Kopito R.R., Andersson M., Lodish H.F.;  
 RT "Structure and organization of the murine band 3 gene.";  
 RL J. Biol. Chem. 262:8035-8040(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX Kopito R.R.;  
 RL Submitted (JUL-1987) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 11-929 FROM N.A.  
 RX MEDLINE=86274622; PubMed=3015590;

RA Demuth D.R., Shove L.C., Ballantine M., Palumbo A., Fraser P.J.,  
 RA Cloue L., Roversa G., Curtis P.J.;  
 RA "Cloning and structural characterization of a human non-erythroid  
 band 3-like protein.";  
 RL EMBO J. 5:1205-1214(1986).  
 [6]  
 RN SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.  
 RX MEDLINE=89229233; PubMed=2713407;  
 RA Ralda M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,  
 RA Passow H.;  
 RA "Major proteolytic fragments of the murine band 3 protein as obtained  
 after in situ proteolysis";  
 RL Biochim. Biophys. Acta 980:291-298(1989).  
 CC -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE  
 CC ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS  
 CC INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS  
 CC THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING  
 CC SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND  
 CC HEMOGLOBIN.  
 CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 CC AND APPEARS TO BE TETRAMERIC.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=Erythrocyte;  
 CC IsoId=P04919-1; Sequence=Displayed;  
 CC Name=Kidney;  
 CC IsoId=P04919-2; Sequence=VSP\_000454;  
 CC -1- TISSUE SPECIFICITY: ERYTHROCYTE.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC  
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 CC  
 DR EMBL; X02677; CAA26506.1; -;  
 DR EMBL; M29379; AAA37187.1; -;  
 DR EMBL; J02756; AAA37278.1; -;  
 DR EMBL; X03917; CAA27555.1; -;  
 DR PIR; A25314; A25314.  
 DR HSP; P02730; IBTS.  
 DR MGD; MGI:109393; Sic4al.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;  
 KW Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 422 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 423 443 POTENTIAL.  
 FT TRANSMEM 456 475 POTENTIAL.  
 FT TRANSMEM 479 498 POTENTIAL.  
 FT TRANSMEM 510 529 POTENTIAL.  
 FT TRANSMEM 542 560 POTENTIAL.  
 FT TRANSMEM 561 586 EXOPLASMIC LOOP (POTENTIAL).  
 FT DOMAIN 587 606 POTENTIAL.  
 FT TRANSMEM 607 621 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 622 642 POTENTIAL.  
 FT TRANSMEM 643 678 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 679 698 POTENTIAL.  
 FT TRANSMEM 717 737 POTENTIAL.  
 FT TRANSMEM 781 798 POTENTIAL.  
 FT TRANSMEM 803 824 POTENTIAL.  
 FT TRANSMEM 862 883 POTENTIAL.  
 FT CARBOHYD 660 N-LINKED (GLCNAC. . .) (PROBABLE).

FT LIPID 861 861 PALMITATE (BY SIMILARITY).  
 FT VARSPLIC 1 79 Missing (in isoform kidney).  
 FT CONFLICT 467 467 /FTid=VSP\_000454.  
 FT SEQUENCE 929 AA; 103135 MW; 5C0E281C394FB614 CRC64;  
 SQ  
 Query Match 100.0%; Score 104; DB 1; Length 929;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GMPWLSATTVRSVTHANALT 20  
 DQ 738 GMPWLSATTVRSVTHANALT 757  
 RESULT 4  
 B3AT\_CHICK STANDARD; PRT; 922 AA.  
 ID B3AT\_CHICK  
 AC P15575;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Band 3 anion transport protein.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89039870; PubMed=3185555;  
 RA Kim H.R.C., Yew N.S., Ansoerge W., Voss H., Schwager C.,  
 RA Vennstroem B., Zenke M., Engel J.D.;  
 RT "Two different mRNAs are transcribed from a single genomic locus  
 encoding the chicken erythrocyte anion transport proteins (band 3).";  
 RL Mol. Cell. Biol. 8:4416-4424(1988).  
 CC -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE  
 CC ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS  
 CC INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS  
 CC THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING  
 CC SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND  
 CC HEMOGLOBIN.  
 CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 CC AND APPEARS TO BE TETRAMERIC.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: ERYTHROCYTE.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC  
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 CC  
 DR EMBL; M23404; AAA48753.1; -;  
 DR HSP; P02730; IBTS.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.  
 FT DOMAIN 1 416 MEMBRANE (ANION EXCHANGE).  
 FT DOMAIN 417 922 POTENTIAL.  
 FT TRANSMEM 417 437 POTENTIAL.  
 FT TRANSMEM 450 469 POTENTIAL.  
 FT TRANSMEM 473 492 POTENTIAL.  
 FT TRANSMEM 504 523 POTENTIAL.  
 FT TRANSMEM 536 554 POTENTIAL.

FT DOMAIN 555 579 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 580 599 POTENTIAL.  
 FT DOMAIN 600 614 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 615 635 POTENTIAL.  
 FT DOMAIN 636 671 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 672 691 POTENTIAL.  
 FT TRANSMEM 710 730 POTENTIAL.  
 FT TRANSMEM 774 791 POTENTIAL.  
 FT TRANSMEM 796 817 POTENTIAL.  
 FT TRANSMEM 855 876 POTENTIAL.  
 FT CARBOHYD 653 653 N-LINKED (GLCNAC... ) (PROBABLE).  
 SQ SEQUENCE 922 AA; 102223 MW; FF4ECAD6D60CF0CF CRC64;

Query Match 96.2%; Score 100; DB 1; Length 922;

Best Local Similarity 90.0%; Pred. No. 2e-08; Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20

DB 731 GMPWLSATTVRTITHANALT 750

# RESULT 5

ID B3AT\_ONCMY STANDARD; PRT; 918 AA.

AC P32847;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Band 3 anion exchange protein.  
 GN SLC4A1 OR AEL.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92344566; PubMed=1637296;  
 RA Hubner S., Michel F., Rudloff V., Appelbans H.;  
 RT "Amino acid sequence of band-3 protein from rainbow trout  
 erythrocytes derived from cDNA.";  
 RL Biochem. J. 285:17-23(1992).

CC -1- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN  
 MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,  
 WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR  
 CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).  
 CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 AND APPEARS TO BE TETRAMERIC (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

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 CC -----

DR EMBL; X61699; CAA43868.1; -  
 DR PIR; S24318; S24318.  
 DR HSR; P02730; IEPQ.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Anion exchange; Lipoprotein; Palmitate.  
 FT DOMAIN 1 392 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 393 918 MEMBRANE (ANION EXCHANGE).

FT TRANSMEM 393 413 POTENTIAL.  
 FT TRANSMEM 426 445 POTENTIAL.  
 FT TRANSMEM 449 468 POTENTIAL.  
 FT TRANSMEM 480 499 POTENTIAL.  
 FT TRANSMEM 512 530 POTENTIAL.  
 FT DOMAIN 531 581 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 582 601 POTENTIAL.  
 FT DOMAIN 602 616 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 617 637 POTENTIAL.  
 FT DOMAIN 638 673 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 674 693 POTENTIAL.  
 FT TRANSMEM 712 732 POTENTIAL.  
 FT TRANSMEM 772 789 POTENTIAL.  
 FT TRANSMEM 794 815 POTENTIAL.  
 FT TRANSMEM 853 874 POTENTIAL.  
 FT LIPID 852 852 PALMITATE (BY SIMILARITY).  
 FT CARBOHYD 546 546 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 568 568 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 918 AA; 101893 MW; 37E163141FBDC16A CRC64;

Query Match 91.3%; Score 95; DB 1; Length 918;

Best Local Similarity 90.0%; Pred. No. 1.3e-07; Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20

DB 733 GVPWLSAATVRSVTHANALT 752

# RESULT 6

ID B3A2\_RAT STANDARD; PRT; 1234 AA.

AC P23347;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).  
 GN SLC4A2 OR AE2 OR B3RP2.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Stomach;  
 RX MEDLINE=90094439; PubMed=2294114;  
 RA Kudrycki K.E., Newman P.R., Shull G.E.;  
 RT "cDNA cloning and tissue distribution of mRNAs for two proteins that  
 are related to the band 3 Cl-/HCO3-exchanger.";  
 RL J. Biol. Chem. 265:462-471(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90319095; PubMed=2371270;  
 RA Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,  
 RA Kopito R.R.;  
 RT "Functional expression and subcellular localization of an anion  
 exchanger cloned from choroid plexus.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).  
 CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE  
 DISTRIBUTION.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

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 CC -----

DR EMBL; J05166; AAA40799.1; -

DR PIR; A34911; A34911.  
 DR HSP; P02730; 1BTO.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 KW Anion exchange; Lipoprotein; Palmitate.  
 FT DOMAIN 1 704 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 705 1234 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 705 728 POTENTIAL.  
 FT TRANSMEM 734 771 POTENTIAL.  
 FT TRANSMEM 791 813 POTENTIAL.  
 FT TRANSMEM 823 844 POTENTIAL.  
 FT DOMAIN 823 893 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 894 911 POTENTIAL.  
 FT DOMAIN 912 926 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 927 947 POTENTIAL.  
 FT TRANSMEM 981 1003 POTENTIAL.  
 FT TRANSMEM 1029 1050 POTENTIAL.  
 FT TRANSMEM 1084 1129 POTENTIAL.  
 FT TRANSMEM 1156 1192 POTENTIAL.  
 FT DOMAIN 5 317 PRO-RICH.  
 FT DOMAIN 74 88 HIS-RICH.  
 FT CARBOHYD 856 856 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 1166 1166 PALMITATE (BY SIMILARITY).  
 FT CONFLICT 206 206 G -> A (IN REF. 2).  
 FT CONFLICT 925 926 RR -> PG (IN REF. 2).  
 FT CONFLICT 1018 1018 M -> I (IN REF. 2).  
 FT CONFLICT 1156 1156 M -> I (IN REF. 2).  
 SQ SEQUENCE 1234 AA; 136635 MW; FAB4ED12BB916216 CRC64;

Query Match 89.4%; Score 93; DB 1; Length 1234;  
 Best Local Similarity 85.0%; Pred. No. 3.7e-07;  
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GMPWLSATTVRSVTHANALT 20  
 !:!!!!:!!!!!!  
 Db 1043 GLPWLAATAVRSVTHANALT 1062

RESULT 7  
 B3A2\_MOUSE STANDARD; PRT; 1237 AA.  
 AC P13808; Q9ES09; Q9ES10; Q9ES11; Q9ES12; Q9ES13;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).  
 GN SLC4A2 OR AE2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RX MEDLINE=89034212; PubMed=3182834;  
 RA Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;  
 RT "Cloning and characterization of a murine band 3-related cDNA from  
 kidney and from a lymphoid cell line.";  
 RL J. Biol. Chem. 263:17092-17099(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
 RX MEDLINE=20462926; PubMed=11006093;  
 RA Lecanda J., Urtasun R., Medina J.F.;  
 RT "Molecular cloning and genomic organization of the mouse AE2 anion  
 exchanger gene.";  
 RL Biochem. Biophys. Res. Commun. 276:117-124(2000).

CC CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE  
 CC CC DISTRIBUTION.  
 CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC CC -!- ALTERNATIVE PRODUCTS:  
 CC CC Event-Alternative splicing; Named isoforms=5;  
 CC CC Name=A;  
 CC CC IsoId=PI13808-1; Sequence=Displayed;  
 CC CC Name=B1;  
 CC CC IsoId=PI13808-2; Sequence=VSP\_000458;  
 CC CC Name=B2;  
 CC CC IsoId=PI13808-3; Sequence=VSP\_000457;  
 CC CC Name=C1;  
 CC CC IsoId=PI13808-4; Sequence=VSP\_000460;  
 CC CC Name=C2;  
 CC CC IsoId=PI13808-5; Sequence=VSP\_000459, VSP\_000461;  
 CC CC TISSUE SPECIFICITY: Isoform a is widely expressed at similar  
 CC CC levels in all tissues examined. Isoforms b1 and b2 are  
 CC CC predominantly expressed in stomach although they are also detected  
 CC CC at lower levels in other tissues. Isoform c1 is stomach-specific.  
 CC CC Isoform c2 is expressed at slightly higher levels in lung and  
 CC CC stomach than in other tissues.  
 CC CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
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 CC CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC CC -----  
 CC CC EMBL; J04036; AAA65505.1; -  
 CC CC EMBL; AF255774; AAG23154.1; -  
 CC CC EMBL; AF255774; AAG23155.1; -  
 CC CC EMBL; AF255774; AAG23156.1; -  
 CC CC EMBL; AF255774; AAG23158.1; -  
 CC CC EMBL; AF255774; AAG23157.1; -  
 CC CC PIR; A31789; A31789.  
 CC CC HSP; P02730; 1BTO.  
 CC CC MGD; MGI:109351; Slc4a2.  
 CC CC InterPro; IPR001717; Anion\_exchange.  
 CC CC InterPro; IPR003020; HCO3\_cotranspt.  
 CC CC Pfam; PF00955; HCO3\_cotransp; 1.  
 CC CC PRINTS; PR01231; HCO3TRNSPORT.  
 CC CC TIGRFAMS; TIGR00834; ae; 1.  
 CC CC PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 CC CC PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 KW Anion exchange; Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 703 MEMBRANE (ANION EXCHANGE).  
 FT DOMAIN 704 1237 POTENTIAL.  
 FT TRANSMEM 704 727 POTENTIAL.  
 FT TRANSMEM 733 770 POTENTIAL.  
 FT TRANSMEM 790 812 POTENTIAL.  
 FT TRANSMEM 822 843 POTENTIAL.  
 FT DOMAIN 844 896 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 897 914 POTENTIAL.  
 FT DOMAIN 915 929 POTENTIAL.  
 FT TRANSMEM 930 950 POTENTIAL.  
 FT TRANSMEM 984 1006 POTENTIAL.  
 FT TRANSMEM 1032 1053 POTENTIAL.  
 FT TRANSMEM 1087 1132 POTENTIAL.  
 FT TRANSMEM 1159 1195 POTENTIAL.  
 FT DOMAIN 5 316 PRO-RICH.  
 FT DOMAIN 73 87 HIS-RICH.  
 FT DOMAIN 861 865 POLY-SER.  
 FT CARBOHYD 855 855 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 1169 1169 PALMITATE (BY SIMILARITY).  
 FT VARSPLIC 1 17 MSSAPRRPASGADSLHT -> MDELLRPQ (in isoform  
 FT B2).  
 FT /ftid=vsp\_000457.

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FT  VARSPLIC 1 17 MSSAPRRPAGADSLHT -> MTQ (in isoform B1).
FT  /FTID=VSP_000458.
FT  VARSPLIC 1 166 Missing (in isoform C2).
FT  /FTID=VSP_000459.
FT  VARSPLIC 1 198 Missing (in isoform C1).
FT  /FTID=VSP_000460.
FT  VARSPLIC 167 193 ERTSPSPPTTPHGEAARASKGAQTG -> MPAFQEWKSG
FT  GLREAVFGAGCSVCR (in isoform C2).
FT  /FTID=VSP_000461.
FT  CONFLICT 205 205 A -> G (IN REF. 2).
FT  SEQUENCE 1237 AA; 136813 MW; 1A0782C0071782EE CRC64;

Query Match      89.4%; Score 93; DB 1; Length 1237;
Best Local Similarity 85.0%; Pred. No. 3.7e-07;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20
Db 1046 GLPWLAATVRSVTHANALT 1065

RESULT 8
B3A2_RABIT
ID B3A2_RABIT STANDARD; PRT; 1237 AA.
AC P48746;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
GN SLC4A2 OR AE2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=3035730; PubMed=1415547;
RA Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;
RT "cDNA cloning and localization of a band 3-related protein from
RL ileum."
RL Am. J. Physiol. 263:G345-G352(1992).
CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC
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CC
CC EMBL; S45791; AAB23488.1; -.
CC PIR; A56764; A56764.
CC HSSP; P02730; 1BTO.
CC InterPro; IPR001717; Anion_exchange.
CC InterPro; IPR003020; HCO3_cotransp.
CC Pfam; PF00955; HCO3_cotransp; 1.
CC PRINTS; PR01231; HCO3TRNSPORT.
CC TIGRFS; TIGR00834; ae; 1.
CC PROSITE; PS00219; ANION_EXCHANGER_1; 1.
CC PROSITE; PS00220; ANION_EXCHANGER_2; 1.
CC Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
CC Anion exchange; Lipoprotein; Palmitate.
CC CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 703
FT 704 1237 MEMBRANE (ANION EXCHANGE).
FT 704 1237
FT 704 727
FT 733 770
FT 790 812
FT 822 843
FT 843

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FT  DOMAIN 844 896 EXOPLASMIC LOOP (POTENTIAL).
FT  TRANSMEM 897 914 POTENTIAL.
FT  DOMAIN 915 929 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 930 950 POTENTIAL.
FT  TRANSMEM 984 1006 POTENTIAL.
FT  TRANSMEM 1032 1053 POTENTIAL.
FT  TRANSMEM 1087 1132 POTENTIAL.
FT  TRANSMEM 1159 1195 POTENTIAL.
FT  DOMAIN 5 316 PRO-RICH.
FT  DOMAIN 74 88 HIS-RICH.
FT  CARBOHYD 855 855 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 864 864 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  LIPID 1169 1169 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 1237 AA; 136535 MW; 2811D11051552BB2 CRC64;

Query Match      89.4%; Score 93; DB 1; Length 1237;
Best Local Similarity 85.0%; Pred. No. 3.7e-07;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20
Db 1046 GLPWLAATVRSVTHANALT 1065

RESULT 9
B3A2_HUMAN
ID B3A2_HUMAN STANDARD; PRT; 1241 AA.
AC P04920; Q969L3;
DT 13-AUG-1987 (Rel. 05, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
GN SLC4A2 OR AE2 OR EPB3L1 OR HKB3 OR MPB3L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=92223115; PubMed=1562608;
RA Gehrig H., Mueller W., Apffelhaus H.;
RT "Complete nucleotide sequence of band 3 related anion transport
RL protein AE2 from human kidney."
RL Biochim. Biophys. Acta 1130:326-328(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Vallon J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Small D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 375-1241 FROM N.A.
RX MEDLINE=86274622; PubMed=3015590;
RA Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,

```

RA Cioe L., Rovera G., Curtis P.J.;  
RT "cloning and structural characterization of a human non-erythroid  
RL band 3-like protein";  
EMBO J. 5:1205-1214(1986).  
CC -|- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE  
CC DISTRIBUTION.  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Comment-Additional isoforms seem to exist;  
CC Name=A;  
CC IsoId=P04920-1; Sequence=Displayed;  
CC Name=B1;  
CC IsoId=P04920-2; Sequence=VSP\_000456;  
CC -|- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
CC -----  
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CC -----  
DR EMBL; X62137; CAA44067.1; -;  
DR EMBL; BC009386; AAB09386.1; -;  
DR EMBL; BC009434; AAB09434.1; -;  
DR EMBL; X03918; CAA27556.1; -;  
DR PIR; S21086; S21086.  
DR HSSP; P02730; IRTQ.  
DR Genew; HGNC:11028; SLC4A2.  
DR MIM; 109280; -;  
DR GO; GO:0005624; C:membrane fraction; TAS.  
DR GO; GO:0008509; F:anion transporter activity; TAS.  
DR GO; GO:0006820; P:anion transport; TAS.  
DR InterPro; IPR001717; Anion\_exchanger.  
DR InterPro; IPR003020; HCO3\_cotransp.  
DR Pfam; PF00955; HCO3\_cotransp; 1.  
DR PRINTS; PR01231; HCO3TRNSPORT.  
DR TIGRFS; TIGR00834; ae; 1.  
DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
KW Anion exchange; Lipoprotein; Palmitate; Alternative splicing.  
FT DOMAIN 1 707 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 708 1241 MEMBRANE (ANION EXCHANGE).  
FT TRANSMEM 708 731 POTENTIAL.  
FT TRANSMEM 737 774 POTENTIAL.  
FT TRANSMEM 784 816 POTENTIAL.  
FT TRANSMEM 826 847 POTENTIAL.  
FT DOMAIN 848 900 EXOPLASMIC LOOP (POTENTIAL).  
FT TRANSMEM 901 918 POTENTIAL.  
FT DOMAIN 919 933 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 934 954 POTENTIAL.  
FT TRANSMEM 988 1010 POTENTIAL.  
FT TRANSMEM 1036 1059 POTENTIAL.  
FT TRANSMEM 1091 1136 POTENTIAL.  
FT TRANSMEM 1163 1199 POTENTIAL.  
FT DOMAIN 5 320 PRO-RICH.  
FT CARBOHYD 859 859 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 868 868 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 882 882 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT LIPID 1173 1173 PALMITATE (BY SIMILARITY).  
FT VARSPLIC 1 17 MSSAPRLPAKGDSFCT -> MTQ (in isoform B1).  
FT FTID=VSP\_000456.  
FT E -> M (IN REF. 1).  
FT H -> R (IN REF. 1).  
FT D -> G (IN REF. 1).  
FT Q -> V (IN REF. 1).  
FT E -> R (IN REF. 1).  
FT MISSING (IN REF. 3).  
FT L -> V (IN REF. 1).  
FT CONFLICT 447 447

FT CONFLICT 450 475 LLGHHGQGAESDPHVTPLMGVPE -> CWGITMVRGLR  
FT VTPSPSLSWELR (IN REF. 3).  
FT EL -> DV (IN REF. 1 AND 3).  
FT AAGAAEDDLRRTRP -> RQQLKMPSADGAA (IN  
FT REF. 1 AND 3).  
FT CONFLICT 824 824 Q -> R (IN REF. 1 AND 3).  
FT CONFLICT 902 902 L -> P (IN REF. 1 AND 3).  
SQ SEQUENCE 1241 AA; 136966 MW; B116908CSA71DB77 CRC64;  
Query Match 89.4%; Score 93; DB 1; Length 1241;  
Best Local Similarity 85.0%; Pred. NO. 3.7e-07;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GMPWLSATTVRSTVTHANALT 20  
DB 1050 GLFWLAATVRSVTHANALT 1069  
:||||:| ||||| |||||  
RESULT 10  
B3A3\_MOUSE  
ID B3A3\_MOUSE STANDARD; PRT; 1227 AA.  
AC P16283;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Anion exchange protein 3 (Neuronal band 3-like protein).  
GN SLC4A3 OR AE3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=90075236; PubMed=2686841;  
RA Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,  
RA Schneider K.;  
RT "Regulation of intracellular pH by a neuronal homolog of the  
RT erythrocyte anion exchanger";  
RL Cell 59:927-937(1989).  
RN [2]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=94171936; PubMed=8126106;  
RA Morgans C.W., Kopito R.R.;  
RT "Generation of truncated brain AE3 isoforms by alternate mRNA  
RT processing";  
RL J. Cell Sci. 106:1275-1282(1993).  
CC -|- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=3;  
CC Name=FL-AE3;  
CC IsoId=P16283-1; Sequence=Displayed;  
CC Name=311-AE3;  
CC IsoId=P16283-2; Sequence=VSP\_000464, VSP\_000465;  
CC Name=14-AE3;  
CC IsoId=P16283-3; Sequence=VSP\_000466, VSP\_000467;  
CC -|- TISSUE SPECIFICITY: NEURONAL.  
CC -|- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
CC -----  
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CC -----  
CC EMBL; M28383; AAA37184.1; -;  
CC EMBL; S69314; AAB30140.1; -;  
CC PIR; A33638; A33638.  
CC HSSP; P02730; IRTQ.  
CC MGD; MGI:109350; SLC4a3.  
CC InterPro; IPR001717; Anion\_exchanger.



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CC EMBL; J05167; AAA40798.1; -  
 DR InterPro: IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 DR Transmembrane; Glycoprotein; Antiport; Ion transport;  
 KW Anion exchange; Lipoprotein; Alternative splicing.  
 KW CYTOPLASMIC.  
 FT DOMAIN 1 707  
 FT TRANSMEM 708 1227  
 FT TRANSMEM 708 730  
 FT TRANSMEM 736 773  
 FT TRANSMEM 793 815  
 FT TRANSMEM 825 846  
 FT TRANSMEM 888 905  
 FT TRANSMEM 906 920  
 FT TRANSMEM 921 941  
 FT TRANSMEM 975 997  
 FT TRANSMEM 1023 1044  
 FT TRANSMEM 1078 1123  
 FT TRANSMEM 1150 1186  
 FT CARBOHYD 868 868  
 FT LIPID 1160 1160  
 FT VARSPPLIC 381 391  
 FT VARSPPLIC 392 1227  
 FT VARSPPLIC 487 503  
 FT VARSPPLIC 504 1227  
 FT VARSPPLIC 1227 AA; 135164 MW; D5BEC46E03F4251C CRG64;  
 Query Match 85.6%; Score 89; DB 1; Length 1227;  
 Best Local Similarity 80.0%; Pred. No. 1.6e-06;  
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GMPWLSATTVRSVTHANALT 20  
 DB 1037 GLPWLTAAATVRSVTHNALT 1056  
 RESULT 11  
 B3A3\_RAT  
 ID B3A3\_RAT STANDARD; PRT; 1227 AA.  
 AC P23348;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Anion exchange protein 3 (Neuronal band 3-like protein).  
 GN SLC4A3 OR AE3 OR B3RF3.  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90094439; PubMed=2294114;  
 RA Kudrycki K.E., Newman P.R., Shull G.E.;  
 RT "cDNA cloning and tissue distribution of mRNAs for two proteins that  
 RT are related to the band 3 Cl-/HCO3-exchanger.";  
 RL J. Biol. Chem. 265:462-471(1990).  
 CC -|- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -|- TISSUE SPECIFICITY: NEURONAL.  
 CC -|- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
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 CC use.

SEQUENCE FROM N.A. (ISOFORM CAE3).

RP TISSUE-Heart;

RA Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;

RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE

CC DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-)

CC EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT

CC CL(-).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Comment-Additional isoforms seem to exist;

CC Name=BAE3;

CC IsoId=P48751-1; Sequence=Displayed;

CC Name=CAE3;

CC IsoId=P48751-2; Sequence=VSP\_000462, VSP\_000463;

CC -1- TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING

CC VENTRICLE.

CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

CC -----

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CC -----

CC ENBL; U05596; AAA50748.1; -

CC EMBL; L27213; AAB05850.1; -

CC PIR; I38496; I38496.

CC HSP; P02730; IRTQ.

CC Genew; HGNC:11029; SLC4A3.

CC MM; 106195; -

CC GO; GO:0005887; C:integral to plasma membrane; TAS.

CC GO; GO:0005624; C:membrane fraction; TAS.

CC GO; GO:0005452; F:inorganic anion exchanger activity; TAS.

CC GO; GO:0006832; P:small molecule transport; TAS.

CC InterPro; IPR001717; Anion\_exchanger.

CC InterPro; IPR003020; HCO3\_cotransp.

CC Pfam; PF00955; HCO3\_cotransp; 1.

CC PRINTS; PR01231; HCO3TRNSPORT.

CC TIGRfams; TIGR00834; ae; 1.

CC PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.

CC PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

CC Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;

CC Anion exchange; Lipoprotein; Palmitate; Alternative splicing.

CC DOMAIN 1 708 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 709 1232 MEMBRANE (ANION EXCHANGE).

CC TRANSMEM 709 731 POTENTIAL.

CC TRANSMEM 737 774 POTENTIAL.

CC TRANSMEM 794 816 POTENTIAL.

CC TRANSMEM 826 847 POTENTIAL.

CC TRANSMEM 893 910 POTENTIAL.

CC DOMAIN 911 925 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 926 946 POTENTIAL.

CC TRANSMEM 980 1002 POTENTIAL.

CC TRANSMEM 1028 1049 POTENTIAL.

CC TRANSMEM 1083 1128 POTENTIAL.

CC TRANSMEM 1155 1191 POTENTIAL.

CC DOMAIN 136 149 POLY-GLU.

CC DOMAIN 152 161 PRO-RICH.

CC DOMAIN 202 207 POLY-SER.

CC DOMAIN 308 313 POLY-LYS.

CC DOMAIN 442 445 POLY-SER.

CC DOMAIN 1184 1187 POLY-LEU.

CC LIPID 1165 1165 PALMITATE (BY SIMILARITY).

CC VARSPPLIC 1 296 Missing (in isoform CAE3).

CC FTID=VSP\_000462.

CC SPS -> MPA (in isoform CAE3).

CC I -> V (IN REF. 2).

CC R -> P (IN REF. 2).

FT CONFLICT 466 466 P -> S (IN REF. 2).

FT CONFLICT 608 608 S -> G (IN REF. 2).

FT CONFLICT 702 702 D -> A (IN REF. 2).

FT CONFLICT 813 813 GS -> FI (IN REF. 2).

FT CONFLICT 822 822 F -> L (IN REF. 2).

FT CONFLICT 861 861 A -> S (IN REF. 2).

FT CONFLICT 867 867 EGSLA -> D (IN REF. 2).

FT CONFLICT 875 875 S -> C (IN REF. 2).

FT CONFLICT 885 885 R -> G (IN REF. 2).

FT CONFLICT 887 887 R -> E (IN REF. 2).

FT CONFLICT 899 899 L -> P (IN REF. 2).

FT CONFLICT 1096 1096 I -> M (IN REF. 2).

SQ SEQUENCE 1232 AA; 135706 MW; 1825BEL5977C3821 CRC64;

Query Match 85.6%; Score 89; DB 1; Length 1232;

Best Local Similarity 80.0%; Pred. No. 1.6e-06;

Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GMPWLSATTVRSVTHNALT 20

Db 1042 GLPWLTAATVRSVTHNALT 1061

RESULT 13

B3A3\_RABIT STANDARD; PRT; 1233 AA.

AC 018917;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Anion exchange protein 3 (Neuronal band 3-like protein) (Anion

DE exchanger 3 brain isoform).

GN SLC4A3 OR AE3.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RP SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RA Abuladze N., Pushkin A., Kurtz I.;

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

CC -----

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CC -----

CC EMBL; AF031650; AAB86859.1; -

CC HSP; P02730; IRTQ.

CC InterPro; IPR001717; Anion\_exchanger.

CC InterPro; IPR003020; HCO3\_cotransp.

CC Pfam; PF00955; HCO3\_cotransp; 1.

CC PRINTS; PR01231; HCO3TRNSPORT.

CC TIGRfams; TIGR00834; ae; 1.

CC PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.

CC PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

CC Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;

CC Anion exchange; Lipoprotein; Palmitate;

CC DOMAIN 1 709 CYTOPLASMIC.

CC DOMAIN 710 1233 MEMBRANE (ANION EXCHANGE).

CC TRANSMEM 710 732 POTENTIAL.

CC TRANSMEM 738 775 POTENTIAL.

CC TRANSMEM 795 817 POTENTIAL.

CC TRANSMEM 827 848 POTENTIAL.

CC TRANSMEM 894 911 POTENTIAL.

FT	DOMAIN	912	926	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	927	947	POTENTIAL.
FT	TRANSMEM	981	1003	POTENTIAL.
FT	TRANSMEM	1029	1050	POTENTIAL.
FT	TRANSMEM	1084	1129	POTENTIAL.
FT	TRANSMEM	1156	1192	POTENTIAL.
FT	CARBOHYD	874	874	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID	1166	1166	PALMITATE (BY SIMILARITY).
FT	DOMAIN	74	83	HIS-RICH.
FT	DOMAIN	136	150	POLY-GLU.
FT	DOMAIN	203	208	POLY-SER.
FT	DOMAIN	309	312	POLY-LYS.
FT	DOMAIN	443	446	POLY-SER.
FT	DOMAIN	1185	1188	POLY-LEU.
SQ	SEQUENCE	1233 AA;	135759 MW; AE486423E9818583 CRC64;	
Query Match 85.6%; Score 89; DB 1; Length 1233;				
Best Local Similarity 80.0%; Pred. No. 1.6e-06;				
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;				
QY	1 GMPWLSATTVRSVTHANALT 20			
DB	1043 GLPWLTAAATVRSVTHVNAIT 1062			
RESULT 14				
ID	B3A2_CAVPO	STANDARD;	PRT; 1238 AA.	
AC	Q920S8;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2			
DE	anion exchanger).			
GN	SLC4A2 OR AE2.			
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.			
OX	NCBI_TaxID=10141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NIH 2; TISSUE=Organ of Corti;			
RX	MEDLINE=99023787; PubMed=9804866;			
RA	Mhatre A.N., Charachon G., Alper A.L., Lalwani A.K.;			
RT	"The guinea pig cochlear AE2 anion exchanger: cDNA cloning and in situ			
RT	localization within the cochlea";			
RL	Biochim. Biophys. Acta 1414:1-15(1998).			
CC	-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE			
CC	DISTRIBUTION.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.			
CC				
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC				
DR	EMBL; AF121253; AAD19700.1; -			
DR	HSSP; P02730; 1BQ.			
DR	InterPro; IPR001717; Anion exchange.			
DR	InterPro; IPR003020; HCO3_cotranspt.			
DR	Pfam; PF00955; HCO3_cotransp; 1.			
DR	PRINTS; PRO1231; HCO3TRNSPT.			
DR	TIGRFAMS; TIGR00834; ae; 1.			
DR	PROSITE; PS00219; ANION_EXCHANGER_1; 1.			
DR	PROSITE; PS00220; ANION_EXCHANGER_2; 1.			
KW	Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;			
KW	Anion exchange; Lipoprotein; Palmitate.			
FT	DOMAIN	1	704	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	705	1238	MEMBRANE (ANION EXCHANGE).

FT	TRANSMEM	705	728	POTENTIAL.
FT	TRANSMEM	734	771	POTENTIAL.
FT	TRANSMEM	791	813	POTENTIAL.
FT	TRANSMEM	823	844	POTENTIAL.
FT	DOMAIN	845	897	EXOPLASMIC LOOP (POTENTIAL).
FT	TRANSMEM	898	915	POTENTIAL.
FT	DOMAIN	916	930	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	931	951	POTENTIAL.
FT	TRANSMEM	985	1007	POTENTIAL.
FT	TRANSMEM	1033	1054	POTENTIAL.
FT	TRANSMEM	1088	1133	POTENTIAL.
FT	TRANSMEM	1160	1196	POTENTIAL.
FT	DOMAIN	5	316	PRO-RICH.
FT	DOMAIN	74	88	HIS-RICH.
FT	CARBOHYD	856	856	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	865	865	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	879	879	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID	1170	1170	PALMITATE (BY SIMILARITY).
SQ	SEQUENCE	1238 AA;	137358 MW; FA1739862ED5ADBF CRC64;	
Query Match 79.8%; Score 83; DB 1; Length 1238;				
Best Local Similarity 80.0%; Pred. No. 1.6e-05;				
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;				
QY	1 GMPWLSATTVRSVTHANALT 20			
DB	1047 GLLMLAAATVRSVTHANALT 1066			
RESULT 15				
ID	B3A4_RABIT	STANDARD;	PRT; 955 AA.	
AC	Q9GKY1; Q9GKY2;			
DT	15-SEP-2003 (Rel. 42, Created)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Anion exchange protein 4 (Anion exchanger 4).			
GN	SLC4A9 OR AE4.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND			
RC	CHARACTERIZATION.			
RC	TISSUE=Kidney.			
RX	MEDLINE=21269379; PubMed=11102437;			
RA	Tsuganezawa H., Kobayashi K., Iyori M., Araki T., Koizumi A.,			
RA	Watanabe S.-I., Kaneko A., Fukao T., Monkawa T., Yoshida T., Kim D.K.,			
RA	Kanai Y., Endou H., Hayashi M., Saruta T.;			
RT	"A new member of the HCO3-transporter superfamily is an apical anion			
RT	exchanger of beta-intercalated cells in the kidney.";			
RL	J. Biol. Chem. 276:8180-8189(2001).			
CC	-!- FUNCTION: Probable apical anion exchanger of the beta-intercalated			
CC	cells of kidney. May participate in HCO3(-) secretion.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. In contrast to			
CC	the rat ortholog, it is present on apical membrane of cortical			
CC	kidney cells.			
CC	-!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1; Synonyms=AB4a;			
CC	Isoid=Q9GKY1-1; Sequence=Displayed;			
CC	Name=2; Synonyms=AB4b;			
CC	Isoid=Q9GKY1-2; Sequence=VSP_007088;			
CC	-!- TISSUE SPECIFICITY: Highly expressed in kidney. Expressed in			
CC	certain types of cells in the kidney cortex.			
CC	-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.			
CC				
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			

TRANSMEM	705	728	POTENTIAL.
TRANSMEM	734	771	POTENTIAL.
TRANSMEM	791	813	POTENTIAL.
TRANSMEM	823	844	POTENTIAL.
DOMAIN	845	897	EXOPLASMIC LOOP (POTENTIAL).
TRANSMEM	898	915	POTENTIAL.
DOMAIN	916	930	CYTOPLASMIC (POTENTIAL).
TRANSMEM	931	951	POTENTIAL.
TRANSMEM	985	1007	POTENTIAL.
TRANSMEM	1033	1054	POTENTIAL.
TRANSMEM	1088	1133	POTENTIAL.
TRANSMEM	1160	1196	POTENTIAL.
DOMAIN	5	316	PRO-RICH.
DOMAIN	74	88	HIS-RICH.
CARBOHYD	856	856	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	865	865	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD	879	879	N-LINKED (GLCNAC. . .) (POTENTIAL).
LIPID	1170	1170	PALMITATE (BY SIMILARITY).
SEQUENCE	1238 AA;	137358 MW;	FA1739862ED5ADBF CRC64;
Query Match 79.8%; Score 83; DB 1; Length 1238;			
Best Local Similarity 80.0%; Pred No. 1.6e-05;			
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;			
QY	1 GMPWLSATTVRSVTHANALT 20		
DB	1047 GLLWLAATVRSVTHANALT 1066		
RESULT 15			
ID	B3A4_RABIT	STANDARD;	PRT; 955 AA.
AC	Q9GKY1; Q9GKY2;		
DT	15-SEP-2003 (Rel. 42, Created)		
DT	15-SEP-2003 (Rel. 42, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Anion exchange protein 4 (Anion exchanger 4).		
GN	SLC4A9 OR AE4.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND		
RC	CHARACTERIZATION.		
RC	TISSUE=Kidney.		
RX	MEDLINE=21269379; PubMed=11102437;		
RA	Tsuganezawa H., Kobayashi K., Iyori M., Araki T., Koizumi A.,		
RA	Watanabe S.-I., Kaneko A., Fukao T., Monkawa T., Yoshida T., Kim D.K.,		
RA	Kanai Y., Endou H., Hayashi M., Saruta T.;		
RT	"A new member of the HCO3-transporter superfamily is an apical anion		
RT	exchanger of beta-intercalated cells in the kidney.";		
RL	J. Biol. Chem. 276:8180-8189(2001).		
CC	-!- FUNCTION: Probable apical anion exchanger of the beta-intercalated		
CC	cells of kidney. May participate in HCO3(-) secretion.		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein. In contrast to		
CC	the rat ortholog, it is present on apical membrane of cortical		
CC	kidney cells.		
CC	-!- ALTERNATIVE PRODUCTS:		
CC	Event-Alternative splicing; Named isoforms=2;		
CC	Name=1; Synonyms=AE4a;		
CC	ISOid=Q9GKY1-1; Sequence=Displayed;		
CC	Name=2; Synonyms=AE4b;		
CC	ISOid=Q9GKY1-2; Sequence=VSP_007088;		
CC	-!- TISSUE SPECIFICITY: Highly expressed in kidney. Expressed in		
CC	certain types of cells in the kidney cortex.		
CC	-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.		
CC	-----		
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CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		

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CC -----  
 DR EMBL; AB038263; BAB18935.1; +.  
 DR EMBL; AB038264; BAB18936.1; +.  
 DR HSP; P02730; IBNX.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRANSPORT.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 KW Anion exchange; Alternative splicing.  
 FT DOMAIN 1 386 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 387 955 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 387 407 POTENTIAL.  
 FT TRANSMEM 415 435 POTENTIAL.  
 FT TRANSMEM 438 458 POTENTIAL.  
 FT TRANSMEM 472 492 POTENTIAL.  
 FT TRANSMEM 503 523 POTENTIAL.  
 FT DOMAIN 524 595 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 596 616 POTENTIAL.  
 FT TRANSMEM 637 657 POTENTIAL.  
 FT DOMAIN 658 683 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 684 704 POTENTIAL.  
 FT TRANSMEM 730 750 POTENTIAL.  
 FT TRANSMEM 785 804 POTENTIAL.  
 FT TRANSMEM 847 867 POTENTIAL.  
 FT TRANSMEM 871 891 POTENTIAL.  
 FT CARBOHYD 548 548 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 317 332 Missing (in isoform 2).  
 FT /FTid=VSP\_007088.  
 SQ SEQUENCE 955 AA; 105032 MW; 04E595A2BFC415B7 CRC64;

Query Match 47.18; Score 49; DB 1; Length 955;  
 Best Local Similarity 42.18; Pred. No. 4.2;  
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 GMPWLSATTVRSVTHANAL 19  
 Db 744 GLPWVVSATVLSLAHMDSL 762  
 |::| : || | : |::|

Search completed: September 3, 2003, 11:46:55  
 Job time : 10.25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:25:42 ; Search time 9.25 Seconds  
(without alignments)  
101.679 Million cell updates/sec

Title: US-10-087-464-2

Perfect score: 98

Sequence: 1 SVTHANALTVNGKASTPGAA 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	98	100.0	911	1 B3AT_HUMAN	P02730 homo sapien
2	91	92.9	927	1 B3AT_RAT	P23562 rattus norv
3	91	92.9	929	1 B3AT_MOUSE	P04919 mus musculus
4	73	74.5	1234	1 B3A2_RAT	P23347 rattus norv
5	73	74.5	1237	1 B3A2_MOUSE	P13808 mus musculus
6	73	74.5	1237	1 B3A2_RABIT	P48746 onychomys
7	73	74.5	1238	1 B3A2_CAVPO	P02088 cavia porce
8	73	74.5	1241	1 B3A2_HUMAN	P04920 homo sapien
9	71	72.4	922	1 B3AT_CHICK	P15575 gallus gall
10	63	64.3	918	1 B3AT_ONCMY	P32847 oncorhynch
11	61	62.2	1227	1 B3A3_MOUSE	P16283 mus musculus
12	61	62.2	1227	1 B3A3_RAT	P23348 rattus norv
13	61	62.2	1232	1 B3A3_HUMAN	P48751 homo sapien
14	61	62.2	1233	1 B3A3_RABIT	O18917 onychomys
15	49	50.0	262	1 Y003_HAELIN	P44447 haemophilus
16	48	49.0	1655	1 OMPB_RICCN	P09883 r outer mem
17	47	48.0	1300	1 L20K_RICRI	P14914 rickettsia
18	47	48.0	1654	1 OMPB_RICRI	Q53047 r outer mem
19	42.5	43.4	705	1 NUCL_HUMAN	P19338 homo sapien
20	42	42.9	303	1 FTSY_RICPR	O05948 rickettsia
21	41.5	42.3	495	1 WD21_HUMAN	Q8WV16 homo sapien
22	41	41.8	122	1 YFC5_SHEFR	Q02482 shewanella
23	41	41.8	256	1 TPIS_AGRF5	Q8UEY3 agrobacteri
24	40	40.8	270	1 PANB_OCEIH	O8ELF4 oceanobacil
25	40	40.8	312	1 YEIN_ECOLI	P33025 escherichia
26	40	40.8	568	1 PUR6_CANAL	Q92210 candida alb
27	40	40.8	779	1 Y700_MYCTU	Q10821 mycobacteri
28	40	40.8	874	1 BCAL_MOUSE	Q61140 mus musculus
29	40	40.8	968	1 BCAL_RAT	Q63767 rattus norv
30	39	39.8	190	1 PBP_PLAFA	P54189 plasmodium
31	39	39.8	399	1 BRS3_MOUSE	O54798 mus musculus
32	39	39.8	402	1 ALP_CEPAC	P29118 cephalospor
33	39	39.8	402	1 OPS4_CANAL	P46596 candida alb

## RESULT 1

ID	B3AT_HUMAN	STANDARD:	PRT:	911 AA.
AC	P02730;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Band 3 anion transport protein (Anion exchange protein 1) (AE 1)			
DE	(CD233 antigen).			
GN	SLC4A1 OR AE1 OR EPB3 OR DI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90083213; PubMed=2594752;			
RA	Lux S.E., John K.M., Kopito R.R., Lodish H.F.;			
RT	"Cloning and characterization of band 3, the human erythrocyte anion-exchange protein (AE1)."			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RX	MEDLINE=89134172; PubMed=3223947;			
RA	Tanner M.J.A., Martin P.G., High S.;			
RT	"The complete amino acid sequence of the human erythrocyte membrane anion-transport protein deduced from the cDNA sequence."			
RL	Biochem. J. 256:703-712(1988).			
RN	[3]			
RP	SEQUENCE OF 1-199; 220-292 AND 347-370.			
RX	MEDLINE=90001294; PubMed=2790053;			
RA	Yannoukakos D., Vasseur C., Blouquit Y., Bursaux E., Wajzman H.;			
RT	"Primary structure of the cytoplasmic domain of human erythrocyte protein band 3. Comparison with its sequence in the mouse."			
RL	Biochim. Biophys. Acta 998:43-49(1989).			
RN	[4]			
RP	SEQUENCE OF 1-201.			
RX	MEDLINE=83238395; PubMed=6345535;			
RA	Kaul R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;			
RT	"Amino acid sequence of the N alpha-terminal 201 residues of human erythrocyte membrane band 3."			
RL	J. Biol. Chem. 258:7981-7990(1983).			
RN	[5]			
RP	SEQUENCE OF 1-3.			
RX	MEDLINE=79027186; PubMed=701248;			
RA	Drickamer L.K.;			
RT	"Orientation of the band 3 polypeptide from human erythrocyte membranes. Identification of NH2-terminal sequence and site of carbohydrate attachment."			
RL	J. Biol. Chem. 253:7242-7248(1978).			
RN	[6]			
RP	SEQUENCE OF 559-630.			
RX	MEDLINE=83308584; PubMed=6615451;			
RA	Brock C.J., Tanner M.J.A., Kempf C.;			
RT	"The human erythrocyte anion-transport protein. Partial amino acid			

## ALIGNMENTS

34	39	39.8	529	1 YPCL_CAEEL	Q11178 caenorhabdi
35	39	39.8	662	1 MUC1_XENLA	Q05049 xenopus lae
36	39	39.8	681	1 TBR1_MOUSE	Q64336 mus musculus
37	39	39.8	682	1 TBR1_HUMAN	Q16650 homo sapien
38	39	39.8	776	1 RTN1_HUMAN	Q16799 homo sapien
39	38.5	39.3	356	1 EGSA_METAC	Q8CJUL mechanosarc
40	38.5	39.3	390	1 C3L2_HUMAN	Q15782 homo sapien
41	38.5	39.3	470	1 UL49_HSV6U	P52441 human herpe
42	38	38.8	116	1 B2MG_BRARE	Q04475 brachydanio
43	38	38.8	125	1 RSL3_RICCN	Q929Y8 rickettsia
44	38	38.8	125	1 RSL3_RICPR	Q92CS7 rickettsia
45	38	38.8	276	1 YAKO_BACSU	P94368 bacillus su

sequence, conformation and a possible molecular mechanism for anion exchange.";  
 RL Biochem. J. 213:577-586(1983).  
 RN [7]  
 RP SEQUENCE OF 834-911.  
 RX MEDLINE-88228050; PubMed-3372523;  
 RA Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.;  
 RT "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein.";  
 RL J. Biol. Chem. 263:8232-8238(1988).  
 RN [8]  
 RP ROLE OF GLU-681, AND SEQUENCE OF 665-688.  
 RX MEDLINE-92332495; PubMed-1352774;  
 RA Jennings M.L., Smith J.S.;  
 RT "Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681.";  
 RL J. Biol. Chem. 267:13964-13971(1992).  
 RN [9]  
 RP PALMITOYLATION OF CYS-843.  
 RX MEDLINE-91358422; PubMed-1885574;  
 RA Okubo K., Hamasaki N., Hara K., Kageura M.;  
 RT "Palmitoylation of cysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLAFL found in band 3 protein and G2 protein of Rift Valley fever virus.";  
 RL J. Biol. Chem. 266:16420-16424(1991).  
 RN [10]  
 RP PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.  
 RX MEDLINE-20400020; PubMed-10942405;  
 RA Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E.,  
 RA Pinna L.A., Donella-Deana A.;  
 RT "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites.";  
 RL Blood 96:1550-1557(2000).  
 RN [11]  
 RP VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-91329825; PubMed-1678289;  
 RA Yannoukakos D., Vasseur C., Driancoourt C., Biouquait Y., Delaunay J.,  
 RA Wajzman H., Bursaux E.;  
 RT "Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the structural modification (Lys 56-->Glu) by protein chemistry methods.";  
 RL Blood 78:1117-1120(1991).  
 RN [12]  
 RP VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.  
 RX MEDLINE-92107882; PubMed-1722314;  
 RA Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,  
 RA Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;  
 RT "Deletion in erythrocyte band 3 gene in malaria-resistant Southeast Asian ovalocytosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).  
 RN [13]  
 RP VARIANT HS ARG-327.  
 RX MEDLINE-92329550; PubMed-1378323;  
 RA Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,  
 RA Cohen C.M.;  
 RT "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2.";  
 RL Blood 80:523-529(1992).  
 RN [14]  
 RP VARIANT HE 400-ALA--ALA-408 DEL.  
 RX MEDLINE-92167271; PubMed-1538405;  
 RA Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,  
 RA Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,  
 RA Gratzner W.B.;  
 RT "Basis of unique red cell membrane properties in hereditary ovalocytosis.";  
 RL J. Mol. Biol. 223:949-958(1992).  
 RN [15]  
 RP VARIANT HS LEU-868.  
 RX MEDLINE-93343855; PubMed-83431110;

RA Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;  
 RT "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3.";  
 RL Biochem. J. 293:317-320(1993).  
 RN [16]  
 RP VARIANT MONTEFIORE LYS-40.  
 RX MEDLINE-93229758; PubMed-8471774;  
 RA Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,  
 RA Schwartz R.S.;  
 RT "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore).";  
 RL Blood 81:2155-2165(1993).  
 RN [17]  
 RP VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.  
 RX MEDLINE-94266802; PubMed-8206915;  
 RA Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;  
 RT "Band 3 Memphis variant II. Altered stilbene disulfonate binding and the Diego (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation Pro-854-->Leu.";  
 RL J. Biol. Chem. 269:16155-16158(1994).  
 RN [18]  
 RP VARIANT BLOOD GROUP WR(A).  
 RX MEDLINE-95111140; PubMed-7812009;  
 RA Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,  
 RA Tanner M.J.;  
 RT "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain conditions.";  
 RL Blood 85:541-547(1995).  
 RN [19]  
 RP VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.  
 RX MEDLINE-95134893; PubMed-7530501;  
 RA Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,  
 RA Alper S.L., Brugnara C., Wichterle H., Palek J.;  
 RT "Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis.";  
 RL Blood 85:634-640(1995).  
 RN [20]  
 RP VARIANT HS ASP-771.  
 RX MEDLINE-96136073; PubMed-8547122;  
 RA Maillet P., Vallier A., Reinhardt W.H., Wyss E.J., Ott P., Texier P.,  
 RA Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;  
 RT "Band 3 Chur: a variant associated with band 3-deficient hereditary spherocytosis and substitution in a highly conserved position of transmembrane segment 11.";  
 RL Br. J. Haematol. 91:804-810(1995).  
 RN [21]  
 RP VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.  
 RX MEDLINE-97099297; PubMed-8943874;  
 RA Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T.,  
 RA Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,  
 RA Palek J.;  
 RT "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency.";  
 RL Blood 88:4366-4374(1996).  
 RN [22]  
 RP VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.  
 RX MEDLINE-96225450; PubMed-8640229;  
 RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,  
 RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,  
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";  
 RL Nat. Genet. 13:214-218(1996).  
 RN [23]  
 RP VARIANTS HS SER-147 AND MET-488.  
 RX MEDLINE-97351102; PubMed-9207478;  
 RA Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon M.,  
 RA Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,

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Query Match      100.0%; Score 98; DB 1; Length 911;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVTHANALTVMGKASTPGAA 20
DB      731 SVTHANALTVMGKASTPGAA 750

RESULT 2
B3AT_RAT
ID      B3AT_RAT      STANDARD;      PRT;      927 AA.
AC      P23562;
DT      01-NOV-1991 (Rel. 20, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
GN      SLC4A1 OR AEL.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE OF 46-927 FROM N.A.
RC      TISSUE=Kidney;
RX      MEDLINE=89255254; PubMed=2722777;
RA      Kudrycki K.E., Shull G.E.;
RT      "Primary structure of the rat kidney band 3 anion exchange protein
RT      deduced from a cDNA.";
RL      J. Biol. Chem. 264:8185-8192(1989).
RN      [2]
RP      SEQUENCE OF 1-45 FROM N.A.
RA      Kudrycki K.E., Shull G.E.;
RL      Submitted (XX-1992) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
CC      MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
CC      WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
CC      CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).
CC      -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
CC      AND APPEARS TO BE TETRAMERIC.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
CC      BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
CC      COLLECTING DUCTS.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event-Alternative splicing; Named isoforms=2;
CC      Name=Erythrocyte;
CC      IsoId=P23562-1; Sequence=Displayed;
CC      Name=Kidney;
CC      IsoId=P23562-2; Sequence=VSP_000455;
CC      TISSUE SPECIFICITY: Kidney.
CC      -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      -----
DR      EMBL; J04793; AAA40800.1; ALT-INIT.
DR      EMBL; J02943; AAA40801.1; -.
DR      PIR; A33810; A33810.
DR      HSP; P02730; 1BPS.
DR      InterPro; IPR001717; Anion_exchanger.
DR      InterPro; IPR003020; HCO3_cotransp.
DR      Pfam; PF00955; HCO3_cotransp; 1.
DR      PRINTS; PR01231; HCO3TRNSPORT.
DR      TIGRFAMs; TIGR00834; ae; 1.
DR      PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR      PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW      Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
```

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KW      Lipoprotein; Palmitate; Alternative splicing.
FT      DOMAIN      1      420      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN      421      927      MEMBRANE (ANION EXCHANGE).
FT      TRANSMEM      421      441      POTENTIAL.
FT      TRANSMEM      454      473      POTENTIAL.
FT      TRANSMEM      477      496      POTENTIAL.
FT      TRANSMEM      508      527      POTENTIAL.
FT      TRANSMEM      540      558      POTENTIAL.
FT      DOMAIN      559      585      EXOPLASMIC LOOP (POTENTIAL).
FT      TRANSMEM      585      604      POTENTIAL.
FT      DOMAIN      605      619      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      620      640      POTENTIAL.
FT      DOMAIN      641      676      EXOPLASMIC LOOP (POTENTIAL).
FT      TRANSMEM      677      696      POTENTIAL.
FT      TRANSMEM      715      735      POTENTIAL.
FT      TRANSMEM      779      796      POTENTIAL.
FT      TRANSMEM      801      822      POTENTIAL.
FT      TRANSMEM      860      881      POTENTIAL.
FT      CARBOHYD      658      658      N-LINKED (GLCNAC. . .) (PROBABLE).
FT      LIPID      859      859      PALMITATE (BY SIMILARITY).
FT      VARSPPLIC      1      79      Missing (in isoform kidney).
FT      SEQUENCE      927 AA; 103172 MW; 681A228474E5E9DE CRC64;
SQ      SEQUENCE      927 AA; 103172 MW; 681A228474E5E9DE CRC64;

Query Match      92.9%; Score 91; DB 1; Length 927;
Best Local Similarity 95.0%; Pred. No. 2.2e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SVTHANALTVMGKASTPGAA 20
DB      747 SVTHANALTVMGKASTPGAA 766

RESULT 3
B3AT_MOUSE
ID      B3AT_MOUSE      STANDARD;      PRT;      929 AA.
AC      P04919;
DT      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
DE      (MEB3).
GN      SLC4A1 OR AEL.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=85268011; PubMed=2410791;
RA      Kopito R.R., Lodish H.F.;
RT      "Primary structure and transmembrane orientation of the murine anion
RT      exchange protein.";
RL      Nature 316:234-238(1985).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86034211; PubMed=3840489;
RA      Kopito R.R., Lodish H.F.;
RT      "Structure of the murine anion exchange protein.";
RL      J. Cell. Biochem. 29:1-17(1985).
RN      [3]
RP      PARTIAL SEQUENCE FROM N.A.
RX      MEDLINE=87250387; PubMed=3036795;
RA      Kopito R.R., Andersson M., Lodish H.F.;
RT      "Structure and organization of the murine band 3 gene.";
RL      J. Biol. Chem. 262:8035-8040(1987).
RN      [4]
RP      SEQUENCE FROM N.A.
RA      Kopito R.R.;
RL      Submitted (JUL-1987) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE OF 11-929 FROM N.A.
RX      MEDLINE=86274622; PubMed=3015590;
```

RA Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,  
 RA Cioe L., Rovera G., Curtis P.J.;  
 RT "Cloning and structural characterization of a human non-erythroid  
 RT band 3-like protein.";  
 RL EMBO J. 5:1205-1214(1986).  
 RN [6]  
 RP SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.  
 RX MEDLINE=89229233; PubMed=2713407;  
 RA Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,  
 RA Passow H.;  
 RT "Major proteolytic fragments of the murine band 3 protein as obtained  
 RT after in situ proteolysis.";  
 RL Biochim. Biophys. Acta 980:291-298(1989).  
 CC -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE  
 CC ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS  
 CC INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS  
 CC THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING  
 CC SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND  
 CC HEMOGLOBIN.  
 CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 CC AND APPEARS TO BE TETRAMERIC.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name-Erythrocyte;  
 CC Name-Kidney;  
 CC IsoId=P04919-1; Sequence=Displayed;  
 CC IsoId=P04919-2; Sequence=VSP\_000454;  
 CC -1- TISSUE SPECIFICITY: ERYTHROCYTE.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC  
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 CC  
 CC EMBL; X02677; CAA26506.1; -  
 CC DR EMBL; M29379; AAA37187.1; -  
 CC DR EMBL; J02756; AAA37278.1; -  
 CC DR EMBL; X03917; CAA27555.1; -  
 CC DR PIR; A25314; A25314.  
 CC DR HSP; P02730; IBT.  
 CC DR MGD; MGI:109393; Slc4a1.  
 CC DR InterPro; IPR00117; Anion\_exchange.  
 CC DR Pfam; PF00955; HCO3\_cotransp.  
 CC DR PRINTS; PR01231; HCO3TRANSPORT.  
 CC DR TIGRFS; TIGR00834; ae; 1.  
 CC DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 CC DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 CC DR Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;  
 CC Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 422 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 423 443 POTENTIAL.  
 FT TRANSMEM 456 475 POTENTIAL.  
 FT TRANSMEM 479 498 POTENTIAL.  
 FT TRANSMEM 510 529 POTENTIAL.  
 FT TRANSMEM 542 560 POTENTIAL.  
 FT DOMAIN 561 586 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 587 606 POTENTIAL.  
 FT DOMAIN 607 621 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 622 642 POTENTIAL.  
 FT DOMAIN 643 678 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 679 698 POTENTIAL.  
 FT TRANSMEM 717 737 POTENTIAL.  
 FT TRANSMEM 781 798 POTENTIAL.  
 FT TRANSMEM 803 824 POTENTIAL.  
 FT TRANSMEM 862 883 POTENTIAL.  
 FT CARBOHYD 660 N-LINKED (GLCNAC. . .) (PROBABLE).

FT LIPID 861 861 PALMITATE (BY SIMILARITY).  
 FT VARSPLIC 1 79 Missing (in isoform Kidney).  
 FT FTId=VSP\_000454.  
 FT CONFLICT 467 467 G -> S (IN REF. 5).  
 SQ SEQUENCE 929 AA; 103135 MW; 5C0E281C394FB614 CRC64;  
 Query Match 92.9%; Score 91; DB 1; Length 929;  
 Best Local Similarity 95.0%; Pred. No. 2.2e-07;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 SVTHANALTYMGKASTPGAA 20  
 Db 749 SVTHANALTYMGKASGPGAA 768  
 RESULT 4  
 B3A2\_RAT STANDARD; PRT; 1234 AA.  
 ID B3A2\_RAT  
 AC P23347;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).  
 GN SLCA42 OR AE2 OR B3RP2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Stomach;  
 RX MEDLINE=90094439; PubMed=2294114;  
 RA Kudrycki K.E., Newman P.R., Shull G.E.;  
 RT "cDNA cloning and tissue distribution of mRNAs for two proteins that  
 RT are related to the band 3 CL-/HCO3-exchanger.";  
 RL J. Biol. Chem. 265:462-471(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90319095; PubMed=2371270;  
 RA Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,  
 RA Kopito R.R.;  
 RT "Functional expression and subcellular localization of an anion  
 RT exchanger cloned from choroid plexus.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).  
 CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE  
 CC DISTRIBUTION.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC  
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 CC  
 CC EMBL; J05166; AAA40799.1; -  
 CC PIR; A34911; A34911.  
 CC HSP; P02730; IBTQ.  
 CC InterPro; IPR00117; Anion\_exchange.  
 CC InterPro; IPR003020; HCO3\_cotransp.  
 CC Pfam; PF00955; HCO3\_cotransp; 1.  
 CC PRINTS; PR01231; HCO3TRANSPORT.  
 CC TIGRFS; TIGR00834; ae; 1.  
 CC PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 CC PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 CC Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 CC Anion exchange; Lipoprotein; Palmitate.  
 KW DOMAIN 1 704 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 705 1234 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 705 728 POTENTIAL.



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FT TRANSMEM 734 771 POTENTIAL.
FT TRANSMEM 791 813 POTENTIAL.
FT TRANSMEM 823 844 POTENTIAL.
FT DOMAIN 844 893 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 894 911 POTENTIAL.
FT DOMAIN 912 926 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 927 947 POTENTIAL.
FT TRANSMEM 981 1003 POTENTIAL.
FT TRANSMEM 1029 1050 POTENTIAL.
FT TRANSMEM 1084 1129 POTENTIAL.
FT TRANSMEM 1156 1192 POTENTIAL.
FT DOMAIN 5 317 PRO-RICH.
FT DOMAIN 74 98 HIS-RICH.
FT CARBOHYD 856 856 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 1166 1166 PALMITATE (BY SIMILARITY).
FT CONFLICT 206 206 G -> A (IN REF. 2).
FT CONFLICT 925 926 RR -> PG (IN REF. 2).
FT CONFLICT 1018 1018 M -> I (IN REF. 2).
FT CONFLICT 1156 1156 M -> I (IN REF. 2).
SQ SEQUENCE 1234 AA; 136635 MW; FAB4ED12BB916216 CRC64;

Query Match 74.5%; Score 73; DB 1; Length 1234;
Best Local Similarity 83.3%; Pred. No. 0.00033;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHNALVTMVKASTPG 18
DQ 1054 SVTHNALVTMVKAVPG 1071

RESULT 5
B3A2 MOUSE
ID B3A2 MOUSE STANDARD; PRT: 1237 AA.
AC P13808; Q9ES09; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
GN SLC4A2 OR AE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=89034212; PubMed=3182834;
RA Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
RT "Cloning and characterization of a murine band 3-related cDNA from
RT kidney and from a lymphoid cell line."
RL J. Biol. Chem. 263:17092-17099(1988).
RN [2]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RX MEDLINE=20462926; PubMed=11006093;
RA Lecanda J., Urtaun R., Medina J.F.;
RT "Molecular cloning and genomic organization of the mouse AE2 anion
RT exchanger gene."
RL Biochem. Biophys. Res. Commun. 276:117-124(2000).
CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=5;
CC Name=A;
CC IsoId=PI3808-1; Sequence=Displayed;
CC Name=B1;
CC IsoId=PI3808-2; Sequence=VSP_000458;
CC Name=B2;
CC IsoId=PI3808-3; Sequence=VSP_000457;
CC Name=C1;
CC IsoId=PI3808-4; Sequence=VSP_000460;
CC Name=C2;

CC IsoId=PI3808-5; Sequence=VSP_000459, VSP_000461;
CC -!- TISSUE SPECIFICITY: Isoform A is widely expressed at similar
CC levels in all tissues examined. Isoforms B1 and B2 are
CC predominantly expressed in stomach although they are also detected
CC at lower levels in other tissues. Isoform C1 is stomach-specific.
CC Isoform C2 is expressed at slightly higher levels in lung and
CC stomach than in other tissues.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC
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CC
CC EMBL; J04036; AAA65505.1; -
CC EMBL; AF255774; AAG23154.1; -
CC EMBL; AF255774; AAG23155.1; -
CC EMBL; AF255774; AAG23156.1; -
CC EMBL; AF255774; AAG23158.1; -
CC EMBL; AF255774; AAG23157.1; -
CC PIR; A31789; A31789.
CC HSP; P02730; LBTQ.
CC MGD; MGI:109351; SLC4a2.
CC InterPro; IPR001717; Anion_exchange.
CC InterPro; IPR003020; HCO3_cotransp.
CC Pfam; PF00955; HCO3_cotransp. 1.
CC PRINTS; PR01231; HCO3TRNSPORT.
CC TIGRFS; TIGR00834; ae; 1.
CC PROSITE; PS00219; ANION_EXCHANGER_1; 1.
CC PROSITE; PS00220; ANION_EXCHANGER_2; 1.
CC Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
CC Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
CC DOMAIN 1 703 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 704 1237 MEMBRANE (ANION EXCHANGE).
CC TRANSMEM 704 727 POTENTIAL.
CC TRANSMEM 733 770 POTENTIAL.
CC TRANSMEM 790 812 POTENTIAL.
CC TRANSMEM 822 843 POTENTIAL.
CC DOMAIN 844 896 EXOPLASMIC LOOP (POTENTIAL).
CC TRANSMEM 897 914 POTENTIAL.
CC DOMAIN 915 929 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 930 950 POTENTIAL.
CC TRANSMEM 984 1006 POTENTIAL.
CC TRANSMEM 1032 1053 POTENTIAL.
CC TRANSMEM 1087 1132 POTENTIAL.
CC TRANSMEM 1159 1195 POTENTIAL.
CC DOMAIN 5 316 PRO-RICH.
CC DOMAIN 73 87 HIS-RICH.
CC DOMAIN 861 865 POLY-SER.
CC CARBOHYD 855 855 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC LIPID 1169 1169 PALMITATE (BY SIMILARITY).
CC VARSPIC 1 17 MSSAPRRPASGADSLHT -> MDFLLRPQ (in isoform
CC B2).
CC /FTid=VSP_000457.
CC MSSAPRRPASGADSLHT -> MTQ (in isoform B1).
CC /FTid=VSP_000458.
CC Missing (in isoform C2).
CC /FTid=VSP_000459.
CC Missing (in isoform C1).
CC /FTid=VSP_000460.
CC ERTPSPPTQTHQEAAPRASKGAQTG -> MPAFQEWKSG
CC GLREAVFGAGHCVCVR (in isoform C2).
CC /FTid=VSP_000461.
CC A -> G (IN REF. 2).
CC CONFLICT 205 205 A -> G (IN REF. 2).
CC SEQUENCE 1237 AA; 136813 MW; 1A0782C0071782EE CRC64;

Query Match 74.5%; Score 73; DB 1; Length 1237;
Best Local Similarity 83.3%; Pred. No. 0.00033;

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTYMGRASPTG 18  
 ||||| ||||| || ||

Db 1057 SVTHANALTYMGRASPTG 1074

RESULT 6

B3A2\_RABIT STANDARD; PRT; 1237 AA.

AC P48746;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).

GN SLC4A2 OR AE2.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=New Zealand white;

RX MEDLINE=93035730; PubMed=1415547;

RA Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;

RT "cDNA cloning and localization of a band 3-related protein from ileum.";

RT ileum.";

RL Am. J. Physiol. 263:G345-G352(1992).

CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

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CC EMBL; S45791; AAB23488.1; .

DR PUR; A56764; A56764.

DR HSP; P02730; IBTQ.

DR InterPro; IPR001717; Anion\_exchange.

DR Pfam; PF00955; HCO3\_cotransp; 1.

DR PRINTS; PR01231; HCO3TRANSPORT.

DR TIGRFAMs; TIGR00834; ae; 1.

DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.

DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;

KW Anion exchange; Lipoprotein; Palmitate.

FT DOMAIN 1 703 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 704 1237 MEMBRANE (ANION EXCHANGE).

FT TRANSMEM 704 727 POTENTIAL.

FT TRANSMEM 733 770 POTENTIAL.

FT TRANSMEM 790 812 POTENTIAL.

FT TRANSMEM 822 843 POTENTIAL.

FT DOMAIN 844 896 EXOPLASMIC LOOP (POTENTIAL).

FT TRANSMEM 897 914 POTENTIAL.

FT DOMAIN 915 929 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 930 950 POTENTIAL.

FT TRANSMEM 984 1006 POTENTIAL.

FT TRANSMEM 1032 1053 POTENTIAL.

FT TRANSMEM 1087 1132 POTENTIAL.

FT TRANSMEM 1159 1195 POTENTIAL.

FT DOMAIN 5 316 PRO-RICH.

FT DOMAIN 74 88 HIS-RICH.

FT CARBOHYD 855 855 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 864 864 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT LIPID 1169 1169 PALMITATE (BY SIMILARITY).

SQ SEQUENCE 1237 AA; 136535 MW; 2811D11051552BB2 CRC64;

Query Match 74.5%; Score 73; DB 1; Length 1237;

Best Local Similarity 83.3%; Pred. No. 0.00033;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTYMGRASPTG 18  
 ||||| ||||| || ||

Db 1057 SVTHANALTYMGRASPTG 1074

RESULT 7

B3A2\_CAVPO STANDARD; PRT; 1238 AA.

AC Q920S8;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2 anion exchanger).

DE Anion exchanger).

GN SLC4A2 OR AE2.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI\_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NTH 2; TISSUE=Organ of Corti;

RX MEDLINE=99023787; PubMed=9804866;

RA Matre A.N., Charachon G., Alper A.L., Lalwani A.K.;

RT "The guinea pig cochlear AE2 anion exchanger: cDNA cloning and in situ localization within the cochlea.";

RL Biochim. Biophys. Acta 1414:1-15(1998).

CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

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CC EMBL; AF121253; AAD19700.1; .

DR HSP; P02730; IBTQ.

DR InterPro; IPR001717; Anion\_exchange.

DR Pfam; PF00955; HCO3\_cotransp; 1.

DR PRINTS; PR01231; HCO3TRANSPORT.

DR TIGRFAMs; TIGR00834; ae; 1.

DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.

DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;

KW Anion exchange; Lipoprotein; Palmitate.

FT DOMAIN 1 704 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 705 1238 MEMBRANE (ANION EXCHANGE).

FT TRANSMEM 705 728 POTENTIAL.

FT TRANSMEM 734 771 POTENTIAL.

FT TRANSMEM 791 813 POTENTIAL.

FT TRANSMEM 823 844 POTENTIAL.

FT TRANSMEM 845 897 EXOPLASMIC LOOP (POTENTIAL).

FT TRANSMEM 898 915 POTENTIAL.

FT DOMAIN 916 930 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 931 951 POTENTIAL.

FT TRANSMEM 985 1007 POTENTIAL.

FT TRANSMEM 1033 1054 POTENTIAL.

FT TRANSMEM 1088 1133 POTENTIAL.

FT TRANSMEM 1160 1196 PRO-RICH.

FT DOMAIN 5 316 HIS-RICH.

FT DOMAIN 74 88

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FT CARBOHYD 856 856 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 865 865 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 879 879 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 1170 1170 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 1238 AA; 137358 MW; FA1739862ED5ADBFCRC64;

Query Match 74.5%; Score 73; DB 1; Length 1248;
Best Local Similarity 83.3%; Pred. No. 0.00033;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SVTHANALTVMGKASTGP 18
    |||||
DB 1058 SVTHANALTVMSKAVAPG 1075

RESULT 8
B3A2_HUMAN
ID B3A2_HUMAN STANDARD; PRT; 1241 AA.
AC P04920; Q969L3;
DT 13-AUG-1987 (Rel. 05, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
GN SLC4A2 OR AE2 OR EPB3L1 OR HRB3 OR MPB3L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=92223115; PubMed=1562608;
RA Gehrig H., Mueller W., Appelhans H.;
RT "Complete nucleotide sequence of band 3 related anion transport
RL Biochim. Biophys. Acta 1130:326-328(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 375-1241 FROM N.A.
RX MEDLINE=86274622; PubMed=3015590;
RA Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
RA Cioe L., Roversa G., Curtis P.J.;
RT "Cloning and structural characterization of a human non-erythroid
RL band 3-like protein."
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms seem to exist;

```

Query Match

74.5%; Score 73; DB 1; Length 1241;



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FT DOMAIN 602 616 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 617 637
FT DOMAIN 638 673 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 674 693 POTENTIAL.
FT TRANSMEM 712 732 POTENTIAL.
FT TRANSMEM 772 789 POTENTIAL.
FT TRANSMEM 794 815 POTENTIAL.
FT TRANSMEM 853 874 POTENTIAL.
FT LIPID 852 852 PALMITATE (BY SIMILARITY).
FT CARBOHYD 546 546 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 568 568 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 918 AA; 101893 MW; 37E163141F8DC16A CRC64;

Query Match 64.3%; Score 63; DB 1; Length 918;
Best Local Similarity 76.5%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

Qy 1 SVTHANALTVMGKASTP 17
    |||||
Db 744 SVTHANALTVMGKGP 760

RESULT 11
B3A3_MOUSE STANDARD; PRT; 1227 AA.
AC P16283;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 3 (Neuronal band 3-like protein).
GN SLC4A3 OR AE3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90075236; PubMed=2686841;
RA Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,
RA Schneider K.;
RT "Regulation of intracellular pH by a neuronal homolog of the
RL erythrocyte anion exchanger."
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=94171936; PubMed=8126106;
RA Morgans C.W., Kopito R.R.;
RT "Generation of truncated brain AE3 isoforms by alternate mRNA
processing."
RL J. Cell Sci. 106:1275-1282(1993).
CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=FL-AE3;
CC IsoId=P16283-1; Sequence=Displayed;
CC Name=311-AE3;
CC IsoId=P16283-2; Sequence=VSP_000464, VSP_000465;
CC Name=14-AE3;
CC IsoId=P16283-3; Sequence=VSP_000466, VSP_000467;
CC -!- TISSUE SPECIFICITY: NEURONAL.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M28383; AAA37184.1; -
DR EMBL; S69314; AAB30140.1; -

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DR PIR; A33638; A33638.
DR HSP; P02730; 1BTQ.
DR MGD; MGI:109350; SLC4a3.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRANSPORT.
DR TIGRfams; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 707 CYTOPLASMIC.
FT TRANSMEM 708 1227 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 708 730 POTENTIAL.
FT TRANSMEM 736 773 POTENTIAL.
FT TRANSMEM 793 815 POTENTIAL.
FT TRANSMEM 825 846 POTENTIAL.
FT TRANSMEM 888 905 POTENTIAL.
FT DOMAIN 906 920 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 921 941 POTENTIAL.
FT TRANSMEM 975 997 POTENTIAL.
FT TRANSMEM 1023 1044 POTENTIAL.
FT TRANSMEM 1078 1123 POTENTIAL.
FT TRANSMEM 1150 1186 POTENTIAL.
FT DOMAIN 135 145 POLY-GLU.
FT CARBOHYD 868 868 N-LINKED (GLCNAC... ) (POTENTIAL).
FT LIPID 1160 1160 PALMITATE (BY SIMILARITY).
FT VARSPLIC 381 391 AALLDLEQTL -> RAFWAGNESLL (in isoform
FT 311-AE3).
FT VARSPLIC 392 1227 /FTId=VSP_000464.
FT VARSPLIC 487 503 Missing (in isoform 311-AE3).
FT VARSPLIC 487 503 /FTId=VSP_000465.
FT VARSPLIC 504 1227 KPLHMPGGDGHGKSLK -> FCVLRSPCLGEIVTSGKA
FT VARSPLIC 504 1227 (in isoform 14-AE3).
FT VARSPLIC 504 1227 /FTId=VSP_000466.
FT VARSPLIC 504 1227 Missing (in isoform 14-AE3).
FT VARSPLIC 504 1227 /FTId=VSP_000467.
SQ SEQUENCE 1227 AA; 135164 MW; D5BEC46E03F4251C CRC64;

Query Match 62.2%; Score 61; DB 1; Length 1227;
Best Local Similarity 72.2%; Pred. No. 0.034;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SVTHANALTVMGKASTP 18
    |||||
Db 1048 SVTHNALTVMRTAIPG 1065

RESULT 12
B3A3_RAT STANDARD; PRT; 1227 AA.
AC P23348;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 3 (Neuronal band 3-like protein).
GN SLC4A3 OR AE3 OR B3RP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90094439; PubMed=2294114;
RA Kudrycki K.E., Newman P.R., Shull G.E.;
RT "cDNA cloning and tissue distribution of mRNAs for two proteins that
RT are related to the band 3 Cl-/HCO3-exchanger."
RL J. Biol. Chem. 265:462-471(1990).
CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: NEURONAL.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J05167; AAA40798.1; -.
DR PIR; B34911; B34911.
DR HSP; P02730; lbtQ.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMS; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Lipoprotein; Palmitate.
FT DOMAIN 1 707 CYTOPLASMIC.
FT DOMAIN 708 1227 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 708 730 POTENTIAL.
FT TRANSMEM 736 773 POTENTIAL.
FT TRANSMEM 793 815 POTENTIAL.
FT TRANSMEM 825 846 POTENTIAL.
FT TRANSMEM 888 905 POTENTIAL.
FT DOMAIN 906 920 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 921 941 POTENTIAL.
FT TRANSMEM 975 997 POTENTIAL.
FT TRANSMEM 1023 1044 POTENTIAL.
FT TRANSMEM 1078 1123 POTENTIAL.
FT TRANSMEM 1150 1186 POTENTIAL.
FT CARBOHYD 868 868 N-LINKED (GLCNAC... ) (POTENTIAL).
FT LIPID 1160 1160 PALMITATE (BY SIMILARITY).
FT DOMAIN 74 83 HIS-RICH.
FT DOMAIN 135 149 POLY-GLU.
FT DOMAIN 155 161 POLY-PRO.
FT DOMAIN 307 312 POLY-LYS.
FT DOMAIN 441 444 POLY-SER.
FT DOMAIN 1179 1182 POLY-LEU.
SQ SEQUENCE 1227 AA; 135406 MW; 3EB1620EE011730E CRC64;

Query Match 62.2%; Score 61; DB 1; Length 1227;
Best Local Similarity 72.2%; Pred. No. 0.034;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 SVTHNALTVMGKASTPG 18
Db 1048 SVTHNALTVMRTAIAPG 1065
||||| ||||| |||

RESULT 13
B3A3_HUMAN STANDARD; PRT; 1232 AA.
ID B3A3_HUMAN STANDARD; PRT; 1232 AA.
AC P48751;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain
DE band 3-like protein) (CAE3/BAE3).
GN SLC4A3 OR AE3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BAE3).
RC TISSUE=Heart;
RA MEDLINE=95008042; PubMed=7923606;
RA Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,
Alper, S.L.;

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RT "Molecular cloning, expression, and chromosomal localization of two
RT isoforms of the AE3 anion exchanger from human heart.";
RL Circ. Res. 75:603-614(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM CAE3).
RC TISSUE=Heart;
RA Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;
RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-)
CC EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT
CC CL(-).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=BAE3;
CC IsoId=P48751-1; Sequence=Displayed;
CC Name=CAE3;
CC IsoId=P48751-2; Sequence=VSP_000462, VSP_000463;
CC -!- TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING
CC VENTRICLE.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
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CC -----
DR EMBL; U05596; AAA50748.1; -.
DR EMBL; L27213; AAB05850.1; -.
DR PIR; I38496; I38496.
DR HSP; P02730; lbtQ.
DR Genew; HGNC:11029; SLC4A3.
DR MIM; 106195; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0005452; F:inorganic anion exchanger activity; TAS.
DR GO; GO:0006832; P:small molecule transport; TAS.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMS; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 708 CYTOPLASMIC.
FT DOMAIN 709 1232 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 709 731 POTENTIAL.
FT TRANSMEM 737 774 POTENTIAL.
FT TRANSMEM 794 816 POTENTIAL.
FT TRANSMEM 826 847 POTENTIAL.
FT TRANSMEM 893 910 POTENTIAL.
FT DOMAIN 911 925 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 926 946 POTENTIAL.
FT TRANSMEM 980 1002 POTENTIAL.
FT TRANSMEM 1028 1049 POTENTIAL.
FT TRANSMEM 1083 1128 POTENTIAL.
FT TRANSMEM 1155 1191 POTENTIAL.
FT DOMAIN 136 149 POLY-GLU.
FT DOMAIN 152 161 PRO-RICH.
FT DOMAIN 202 207 POLY-SER.
FT DOMAIN 308 313 POLY-LYS.
FT DOMAIN 442 445 POLY-SER.
FT DOMAIN 1184 1187 POLY-LEU.
FT LIPID 1165 1165 PALMITATE (BY SIMILARITY).
FT VARSPLIC 1 296 Missing (in isoform CAE3).
FT FTId=VSP_000462.

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FT VARSPLIC 297 299 SPS -> MPA (in isoform CAE3).  
 /FTid=VSP\_000463.  
 FT CONFLICT 304 304 I -> V (IN REF. 2).  
 FT CONFLICT 343 343 R -> P (IN REF. 2).  
 FT CONFLICT 466 466 P -> S (IN REF. 2).  
 FT CONFLICT 608 608 S -> G (IN REF. 2).  
 FT CONFLICT 702 702 D -> A (IN REF. 2).  
 FT CONFLICT 812 813 GS -> FI (IN REF. 2).  
 FT CONFLICT 822 822 F -> L (IN REF. 2).  
 FT CONFLICT 861 861 A -> S (IN REF. 2).  
 FT CONFLICT 863 867 EGSLA -> D (IN REF. 2).  
 FT CONFLICT 875 875 S -> C (IN REF. 2).  
 FT CONFLICT 885 885 S -> G (IN REF. 2).  
 FT CONFLICT 887 887 R -> E (IN REF. 2).  
 FT CONFLICT 899 899 L -> P (IN REF. 2).  
 FT CONFLICT 1096 1096 I -> M (IN REF. 2).  
 FT CONFLICT 1232 AA; 135706 MW; 1825BE15977C3821 CRC64;  
 SQ SEQUENCE

Query Match 62.2%; Score 61; DB 1; Length 1232;  
 Best Local Similarity 72.2%; Pred. No. 0.034;  
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPG 18  
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 DB 1053 SVTHYNAITVMTAIPG 1070

## RESULT 14

B3A3\_RABIT  
 ID B3A3\_RABIT STANDARD; PRT; 1233 AA.  
 AC O18917;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Anion exchange protein 3 (Neuronal band 3-like protein) (Anion  
 DE exchanger 3 brain isoform).  
 GN SLC4A3 OR AE3.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Abuladze N., Pushkin A., Kurtz I.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC !- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.  
 CC !- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC !- TISSUE SPECIFICITY: NEURONAL.  
 CC !- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
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 CC  
 DR EMBL; AF031650; AAB86859.1; -.  
 DR HSSP; P02730; 1BTQ.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAWS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_2; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_1; 1.  
 KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 FT DOMAIN 1 709 CYTOPLASMIC.  
 FT DOMAIN 710 1233 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 710 732 POTENTIAL.

FT TRANSMEM 738 775 POTENTIAL.  
 FT TRANSMEM 795 817 POTENTIAL.  
 FT TRANSMEM 827 848 POTENTIAL.  
 FT TRANSMEM 854 911 POTENTIAL.  
 FT DOMAIN 912 926 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 927 947 POTENTIAL.  
 FT TRANSMEM 981 1003 POTENTIAL.  
 FT TRANSMEM 1029 1050 POTENTIAL.  
 FT TRANSMEM 1084 1129 POTENTIAL.  
 FT TRANSMEM 1156 1192 POTENTIAL.  
 FT CARBOHYD 874 874 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT LIPID 1166 1166 PALMITATE (BY SIMILARITY).  
 FT DOMAIN 74 83 HIS-RICH.  
 FT DOMAIN 136 150 POLY-GLU.  
 FT DOMAIN 203 208 POLY-SER.  
 FT DOMAIN 309 312 POLY-LYS.  
 FT DOMAIN 443 446 POLY-SER.  
 FT DOMAIN 1185 1188 POLY-LEU.  
 SQ SEQUENCE 1233 AA; 135759 MW; AE486423E9818583 CRC64;

Query Match 62.2%; Score 61; DB 1; Length 1233;  
 Best Local Similarity 72.2%; Pred. No. 0.034;  
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 SVTHANALTMVGKASTPG 18  
 |||| ||||| | ||  
 DB 1054 SVTHYNAITVMTAIPG 1071

## RESULT 15

Y003\_HAEIN  
 ID Y003\_HAEIN STANDARD; PRT; 262 AA.  
 AC P44447;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Protein HI0003.  
 GN HI0003.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Rd / KW20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
 RT Rd";  
 RL Science 269:496-512(1995).  
 RN [2]  
 RP IDENTIFICATION BY MASS SPECTROMETRY.  
 RX MEDLINE=20137488; PubMed=10675023;  
 RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,  
 RA Gray C., Fountoulakis M.;  
 RT "Two-dimensional map of the proteome of Haemophilus influenzae";  
 RL Electrophoresis 21:411-429(2000).  
 CC !- SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL (E.COLI) / YCSE/YXEH -  
 CC (B.SUBTILIS) FAMILY.  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:25:42 ; Search time 9.25 Seconds  
(without alignments)  
101.679 Million cell updates/sec

Title: US-10-087-464-3  
Perfect score: 96  
Sequence: 1 GKASTPGAAQIQEVKEQRI 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	96	100.0	911	1 B3AT_HUMAN	P02730 homo sapien
2	89	92.7	927	1 B3AT_RAT	P23562 rattus norv
3	89	92.7	929	1 B3AT_MOUSE	P04919 mus musculus
4	61	63.5	922	1 B3AT_CHICK	P15575 gallus gall
5	58	60.4	1234	1 B3A2_RAT	P23347 rattus norv
6	58	60.4	1237	1 B3A2_MOUSE	P13808 mus musculus
7	58	60.4	1237	1 B3A2_RABIT	P48746 oryctolagus
8	58	60.4	1238	1 B3A2_CAVPO	Q92058 cavia porce
9	58	60.4	1241	1 B3A2_HUMAN	P04920 homo sapien
10	54	56.2	1227	1 B3A3_MOUSE	P16283 mus musculus
11	54	56.2	1227	1 B3A3_RAT	P23348 rattus norv
12	54	56.2	1232	1 B3A3_HUMAN	P48751 homo sapien
13	54	56.2	1233	1 B3A3_RABIT	O18917 oryctolagus
14	45	46.9	391	1 RRPB_MOUSE	P16072 mumps virus
15	45	46.9	391	1 RRPB_MOUSE	P16595 mumps virus
16	44	45.8	459	1 NCBI_MOUSE	Q02819 mus musculus
17	44	45.8	459	1 NCBI_RAT	Q63083 rattus norv
18	44	45.8	461	1 NCBI_HUMAN	Q02818 homo sapien
19	43	44.8	323	1 RLOC_ARATH	P57691 arabidopsis
20	43	44.8	452	1 YDJE_ECOLI	P38055 escherichia
21	43	44.8	601	1 CORO_SCHPO	O13923 schizosacch
22	42	43.8	448	1 YNO6_YEAST	P53890 saccharomyc
23	41	42.7	210	1 CAC2_HAECO	P16252 haemochus
24	41	42.7	219	1 BASP_RAT	Q05175 rattus norv
25	41	42.7	265	1 DH47_ARATH	P31168 arabidopsis
26	41	42.7	583	1 FOJO_DROME	P54360 drosophila
27	41	42.7	650	1 VE1_HPV72	Q81999 human papil
28	41	42.7	826	1 VILL_HUMAN	P09327 homo sapien
29	41	42.7	826	1 VILL_MOUSE	Q62468 mus musculus
30	41	42.7	950	1 IF2_LACIC	Q9X764 lactococcus
31	41	42.7	2116	1 MY52_DICDI	P08799 dictyosteli
32	41	42.7	2418	1 SPCA_HUMAN	P02549 homo sapien
33	40.5	42.2	500	1 PROP_ECOLI	P30848 escherichia

34 40.5 42.2 500 1 PROP\_SALTY P40862 salmonella  
35 40.5 42.2 728 1 PKP1\_MOUSE P97350 mus musculus  
36 40 41.7 129 1 RL7\_ANASP Q8Y1J5 anabaena sp  
37 40 41.7 144 1 HAP3\_YEAST P13434 saccharomyc  
38 40 41.7 186 1 RK12\_TOBAC P21929 nicotiana t  
39 40 41.7 444 1 BGHN\_CHLAI Q916X6 chloroflexu  
40 40 41.7 448 1 PRS4\_ORYSA P46466 oryza sativ  
41 40 41.7 453 1 RADA\_CHLPN Q929C8 chlamydia p  
42 40 41.7 463 1 DNRA\_PROS9 O84887 prochloroco  
43 40 41.7 518 1 ATPA\_MYCPN Q50329 mycoplasma  
44 40 41.7 594 1 CIR1\_YEAST Q01649 saccharomyc  
45 40 41.7 594 1 UL93\_HCMVA P16799 human cytom

## ALIGNMENTS

RESULT 1  
B3AT\_HUMAN  
ID B3AT\_HUMAN STANDARD; PRT; 911 AA.  
AC P02730;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)  
DE (CD233 antigen).  
GN SLC4A1 OR AE1 OR EPB3 OR DI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90083213; PubMed=2594752;  
RA Lux S.E., John K.M., Kopito R.R., Lodish H.F.;  
RT "Cloning and characterization of band 3, the human erythrocyte anion-exchange protein (AE1).";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=89134172; PubMed=3223947;  
RA Tanner M.J.A., Martin P.G., High S.;  
RT "The complete amino acid sequence of the human erythrocyte membrane anion-transport protein deduced from the cDNA sequence.";  
RL Biochem. J. 256:703-712(1988).  
RN [3]  
RP SEQUENCE OF 1-199; 220-292 AND 347-370.  
RX MEDLINE=90001294; PubMed=2790053;  
RA Yannoukakos D., Vasseur C., Blouquit Y., Bursaux E., Wajcman H.;  
RT "Primary structure of the cytoplasmic domain of human erythrocyte protein band 3. Comparison with its sequence in the mouse.";  
RL Biochim. Biophys. Acta 998:43-49(1989).  
RN [4]  
RP SEQUENCE OF 1-201.  
RX MEDLINE=83283395; PubMed=6345535;  
RA Kaul R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;  
RT "Amino acid sequence of the N alpha-terminal 201 residues of human erythrocyte membrane band 3.";  
RL J. Biol. Chem. 258:7981-7990(1983).  
RN [5]  
RP SEQUENCE OF 1-3.  
RX MEDLINE=79027186; PubMed=701248;  
RA Drickamer L.K.;  
RT "Orientation of the band 3 polypeptide from human erythrocyte membranes. Identification of NH2-terminal sequence and site of carbohydrate attachment.";  
RL J. Biol. Chem. 253:7242-7248(1978).  
RN [6]  
RP SEQUENCE OF 559-630.  
RX MEDLINE=83308584; PubMed=6615451;  
RA Brock C.J., Tanner M.J.A., Kempf C.;  
RT "The human erythrocyte anion-transport protein. Partial amino acid

sequence, conformation and a possible molecular mechanism for anion exchange." J. Biol. Chem. 263:577-586(1988).  
 [7]  
 RP MEDLINE-88228050; PubMed-3372523;  
 RA Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.;  
 "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein." J. Biol. Chem. 263:8232-8238(1988).  
 [8]  
 RP MEDLINE-92332495; PubMed-1352774;  
 RA Jennings M.L., Smith J.S.;  
 "Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681." J. Biol. Chem. 267:13964-13971(1992).  
 [9]  
 RP PALMITOYLATION OF CYS-843.  
 RA MEDLINE-91358422; PubMed-1885574;  
 RA Okubo K., Hamasaki N., Hara K., Kageura M.;  
 "Palmitoylation of cysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLAIVL found in band 3 protein and G2 protein of Rift Valley fever virus." J. Biol. Chem. 266:16420-16424(1991).  
 [10]  
 RP PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.  
 RA MEDLINE-20400020; PubMed-10942405;  
 RA Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E., Pinna L.A., Donella-Deana A.;  
 "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites." Blood 96:1550-1557(2000).  
 [11]  
 RP VARIANT MEMPHIS GLU-56.  
 RA MEDLINE-91329825; PubMed-1678289;  
 RA Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J., Wajcman H., Bursaux E.;  
 "Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the structural modification (Lys 56-->Glu) by protein chemistry methods." Blood 78:1117-1120(1991).  
 [12]  
 RP VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.  
 RA MEDLINE-92107882; PubMed-1722314;  
 RA Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T., Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;  
 "Deletion in erythrocyte band 3 gene in malaria-resistant Southeast Asian ovalocytosis." Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).  
 [13]  
 RP VARIANT HS ARG-327.  
 RA MEDLINE-92329950; PubMed-1378323;  
 RA Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C., Cohen C.N.;  
 "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2." Blood 80:523-529(1992).  
 [14]  
 RP VARIANT HE 400-ALA--ALA-408 DEL.  
 RA MEDLINE-92167271; PubMed-1538405;  
 RA Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M., Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M., Grätzer W.B.;  
 "Basis of unique red cell membrane properties in hereditary ovalocytosis." J. Mol. Biol. 223:949-958(1992).  
 [15]  
 RP VARIANT HS LEU-868.  
 RA MEDLINE-93343855; PubMed-8343110;

RA Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;  
 "Band 3 HI, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3." Biochem. J. 293:317-320(1993).  
 [16]  
 RP VARIANT MONTEFIORE LYS-40.  
 RA MEDLINE-93229738; PubMed-8471774;  
 RA Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L., Schwartz R.S.;  
 "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore)." Blood 81:2155-2165(1993).  
 [17]  
 RP VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.  
 RA MEDLINE-94266802; PubMed-8206915;  
 RA Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;  
 "Band 3 Memphis variant II. Altered stibene disulfonate binding and the Diego (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation Pro-854-->Leu." J. Biol. Chem. 269:16155-16158(1994).  
 [18]  
 RP VARIANT BLOOD GROUP WR(A).  
 RA MEDLINE-95111140; PubMed-7812009;  
 RA Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S., Tanner M.J.;  
 "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain conditions." Blood 85:541-547(1995).  
 [19]  
 RP VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.  
 RA MEDLINE-95134893; PubMed-7530501;  
 RA Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S., Alper S.L., Brugnara C., Wichterle H., Palek J.;  
 "Mutations of conserved arginines in the membrane domain of erythrocyte band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis." Blood 85:634-640(1995).  
 [20]  
 RP VARIANT HS ASP-771.  
 RA MEDLINE-96136073; PubMed-8547122;  
 RA Maillet P., Vallier A., Reinhardt W.H., Wyss E.J., Ott P., Texier P., Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;  
 "Band 3 Chur: a variant associated with band 3-deficient hereditary spherocytosis and substitution in a highly conserved position of transmembrane segment 11." Br. J. Haematol. 91:804-810(1995).  
 [21]  
 RP VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.  
 RA MEDLINE-97099297; PubMed-8943874;  
 RA Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V., Palek J.;  
 "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency." Blood 88:4366-4374(1996).  
 [22]  
 RP VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.  
 RA MEDLINE-96225450; PubMed-8640229;  
 RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T., Dornweller M., Herbers J., Kugler W., Oezcan R., Pekrun A., Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 "Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis." Nat. Genet. 13:214-218(1996).  
 [23]  
 RP VARIANTS HS SER-147 AND MET-488.  
 RA MEDLINE-97351102; PubMed-9207478;  
 RA Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon M., Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,

```

Query Match      100.0%; Score 96; DB 1; Length 911;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKASTPGAAAIQIEVKQRI 20
    |||||
DB 742 GKASTPGAAAIQIEVKQRI 761

RESULT 2
B3AT_RAT      STANDARD;      PRT;      927 AA.
AC P23562;
DT 01-NOV-1991 (Rel. 20, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
GN SLC4A1 OR AE1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 46-927 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=89255254; PubMed=2722777;
RA Kudrycki K.E., Shull G.E.;
RT "Primary structure of the rat kidney band 3 anion exchange protein
    deduced from a cDNA.";
RL J. Biol. Chem. 264:8185-8192(1989).
RN [2]
RP SEQUENCE OF 1-45 FROM N.A.
RA Kudrycki K.E., Shull G.E.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
    MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
    WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
    CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).
CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
    AND APPEARS TO BE TETRAMERIC.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
    BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
    COLLECTING DUCTS.
CC -1- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=2;
CC Name=Erythrocyte;
CC IsoId=P23562-1; Sequence=Displayed;
CC Name=Kidney;
CC IsoId=P23562-2; Sequence=VSP_000455;
CC -1- TISSUE SPECIFICITY: Kidney.
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
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    modified and this statement is not removed. Usage by and for commercial
    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04793; AAA40800.1; ALT_INIT.
DR EMBL; L02943; AAA40801.1; -.
DR PIR; A33810; A33810.
DR HSPSP; P02730; 1BTS.
DR InterPro; IPR001171; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRANSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
DR Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
KW Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 420 CYTOPLASMIC (POTENTIAL)..
FT DOMAIN 421 927 MEMBRANE (ANION EXCHANGE)..
FT TRANSMEM 421 441 POTENTIAL..
FT TRANSMEM 454 473 POTENTIAL..
FT TRANSMEM 477 496 POTENTIAL..
FT TRANSMEM 508 527 POTENTIAL..
FT TRANSMEM 540 558 POTENTIAL..
FT DOMAIN 559 585 EXOPLASMIC LOOP (POTENTIAL)..
FT TRANSMEM 585 604 POTENTIAL..
FT DOMAIN 605 619 CYTOPLASMIC (POTENTIAL)..
FT TRANSMEM 620 640 POTENTIAL..
FT DOMAIN 641 676 EXOPLASMIC LOOP (POTENTIAL)..
FT TRANSMEM 677 696 POTENTIAL..
FT TRANSMEM 715 735 POTENTIAL..
FT TRANSMEM 779 796 POTENTIAL..
FT TRANSMEM 801 822 POTENTIAL..
FT TRANSMEM 860 881 POTENTIAL..
FT CARBOHYD 658 658 N-LINKED (GLCNAC.. ) (PROBABLE).
FT LIPID 859 859 PALMITATE (BY SIMILARITY).
FT VARSPLIC 1 79 Missing (in isoform Kidney).
FT SEQUENCE 927 AA; 103172 MW; 681A228474E59DE CRC64;

Query Match      92.7%; Score 89; DB 1; Length 927;
Best Local Similarity 95.0%; Pred. No. 3.4e-06;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKASTPGAAAIQIEVKQRI 20
    |||||
DB 758 GKASPGAAAIQIEVKQRI 777

RESULT 3
B3AT_MOUSE
ID B3AT_MOUSE      STANDARD;      PRT;      929 AA.
AC P04919;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
    (MEB3).
GN SLC4A1 OR AE1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85268011; PubMed=2410791;
RA Kopito R.R., Lodish H.F.;
RT "Primary structure and transmembrane orientation of the murine anion
    exchange protein.";
RL Nature 316:234-238(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86034211; PubMed=3840489;
RA Kopito R.R., Lodish H.F.;
RT "Structure of the murine anion exchange protein.";
RL J. Cell. Biochem. 29:1-17(1985).
RN [3]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=87250387; PubMed=3036795;
RA Kopito R.R., Andersson M., Lodish H.F.;
RT "Structure and organization of the murine band 3 gene.";
RL J. Biol. Chem. 262:8035-8040(1987).
RN [4]
RP SEQUENCE FROM N.A.
RA Kopito R.R.;
RL Submitted (JUL-1987) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 11-929 FROM N.A.
RX MEDLINE=86274622; PubMed=3015590;

```

Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cloe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid band 3-like protein."; EMBO J. 5:1205-1214(1986).

[6]

SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.

MEDLINE=89229233; PubMed=2713407;

Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B., Passow H.;

"Major proteolytic fragments of the murine band 3 protein as obtained after in situ proteolysis."; Blochim. Biophys. Acta 980:291-298(1989).

-I- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND HEMOGLOBIN.

CC -I- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein.

CC -I- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=Erythrocyte;

CC IsoId=P04919-1; Sequence=Displayed;

CC Name=Kidney;

CC IsoId=P04919-2; Sequence=VSP\_000454;

CC -I- TISSUE SPECIFICITY: ERYTHROCYTE.

CC -I- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

CC

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CC

EMBL; X02677; CAA36506.1; -

DR EMBL; M29379; AAA37187.1; -

DR EMBL; J02756; AAA37278.1; -

DR EMBL; X03917; CAA27555.1; -

DR PIR; A25314; A25314.

DR HSSP; P02730; 1BTS.

DR MGD; MGI:109393; Slc4a1.

DR InterPro; IPR001717; Anion\_exchange.

DR Pfam; PF00955; HCO3\_cotransp. 1.

DR PRINTS; PR01231; HCO3TRNSPORT.

DR TIGRFAMS; TIGR00834; ae; 1.

DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.

DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;

KW Lipoprotein; Palmitate; Alternative splicing.

FT DOMAIN 1 422 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).

FT TRANSMEM 423 443 POTENTIAL.

FT TRANSMEM 456 475 POTENTIAL.

FT TRANSMEM 479 498 POTENTIAL.

FT TRANSMEM 510 529 POTENTIAL.

FT TRANSMEM 542 560 POTENTIAL.

FT DOMAIN 561 586 EXOPLASMIC LOOP (POTENTIAL).

FT TRANSMEM 587 606 POTENTIAL.

FT DOMAIN 607 621 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 622 642 POTENTIAL.

FT DOMAIN 643 678 EXOPLASMIC LOOP (POTENTIAL).

FT TRANSMEM 679 698 POTENTIAL.

FT TRANSMEM 717 737 POTENTIAL.

FT TRANSMEM 781 798 POTENTIAL.

FT TRANSMEM 803 824 POTENTIAL.

FT TRANSMEM 862 883 POTENTIAL.

FT CARBOHYD 660 660 N-LINKED (GLCNAC. . .) (PROBABLE).

FT LIPID 861 861 PALMITATE (BY SIMILARITY).

FT VARSLIC 1 79 Missing (in isoform Kidney).

FT /FTid=VSP\_000454.

FT CONFLICT 467 467 G -> S (IN REF. 5).

FT SEQUENCE 929 AA; 103135 MW; 5C0E281C394FB614 CRC64;

Query Match 92.7%; Score 89; DB 1; Length 929;

Best Local Similarity 95.0%; Pred. No. 3.4e-06;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GKASTPCAAQIQEVKEQRI 20

Db 760 GRASGPGAAQIQEVKEQRI 779

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RESULT 4

B3AT\_CHICK

ID B3AT\_CHICK STANDARD; PRT; 922 AA.

AC P15575;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Band 3 anion transport protein.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;

OC Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89039870; PubMed=3185555;

RA Kim H.R.C., Yew N.S., Ansoorge W., Voss H., Schwager C., Vannstroom B., Zenke M., Engel J.D.;

RT "Two different mRNAs are transcribed from a single genomic locus encoding the chicken erythrocyte anion transport proteins (band 3)."; Mol. Cell. Biol. 8:4416-4424(1988).

RL -I- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND HEMOGLOBIN.

CC -I- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein.

CC -I- TISSUE SPECIFICITY: ERYTHROCYTE.

CC -I- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

CC

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CC

EMBL; M23404; AAA48753.1; -

DR HSSP; P02730; 1BTO.

DR InterPro; IPR001717; Anion\_exchange.

DR InterPro; IPR003020; HCO3\_cotransp.

DR Pfam; PF00955; HCO3\_cotransp. 1.

DR PRINTS; PR01231; HCO3TRNSPORT.

DR TIGRFAMS; TIGR00834; ae; 1.

DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.

DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.

FT DOMAIN 1 416 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 417 922 MEMBRANE (ANION EXCHANGE).

FT TRANSMEM 417 437 POTENTIAL.

FT TRANSMEM 450 469 POTENTIAL.

FT TRANSMEM 473 492 POTENTIAL.

FT TRANSMEM 504 523 POTENTIAL.

FT TRANSMEM 536 554 POTENTIAL.

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FT DOMAIN 555 579 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 580 599 POTENTIAL.
FT DOMAIN 600 614 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 615 635 POTENTIAL.
FT DOMAIN 636 671 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 672 691 POTENTIAL.
FT TRANSMEM 710 730 POTENTIAL.
FT TRANSMEM 774 791 POTENTIAL.
FT TRANSMEM 796 817 POTENTIAL.
FT TRANSMEM 855 876 POTENTIAL.
FT CARBOHYD 653 653 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 922 AA; 102223 MW; FF4ECAD6D6CFCFCF CRC64;

Query Match 63.5%; Score 61; DB 1; Length 922;
Best Local Similarity 60.0%; Pred. No. 0.087;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GKSTPGAAQIQEVKEQRI 20
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Db 753 GKSAVPGERAHIVEVKEQRL 772

RESULT 5
B3A2_RAT ID B3A2_RAT STANDARD; PRT; 1234 AA.
AC P23347;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
GN SLC4A2 OR AE2 OR B3RP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=90094439; PubMed=2294114;
RA Kudrycki K.E., Newman P.R., Shull G.E.;
RT "cDNA cloning and tissue distribution of mRNAs for two proteins that
RL are related to the band 3 Cl-/HCO3-exchanger.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90319095; PubMed=2371270;
RA Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
RA Kopito R.R.;
RT "Functional expression and subcellular localization of an anion
RL exchanger cloned from choroid plexus.";
RC Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J05166; AAA40799.1;
CC PIR; A34911; A34911.
CC HSP; P02730; 1BTO.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRfams; TIGR00834; ae; 1.

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DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Lipoprotein; Palmitate;
FT DOMAIN 1 704 MEMBRANE (ANION EXCHANGE).
FT DOMAIN 705 1234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 705 728 POTENTIAL.
FT TRANSMEM 734 771 POTENTIAL.
FT TRANSMEM 791 813 POTENTIAL.
FT TRANSMEM 823 844 POTENTIAL.
FT DOMAIN 844 893 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 894 911 POTENTIAL.
FT DOMAIN 912 926 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 927 947 POTENTIAL.
FT TRANSMEM 981 1003 POTENTIAL.
FT TRANSMEM 1029 1050 POTENTIAL.
FT TRANSMEM 1084 1129 POTENTIAL.
FT TRANSMEM 1156 1192 POTENTIAL.
FT DOMAIN 5 317 PRO-RICH.
FT DOMAIN 74 88 HIS-RICH.
FT CARBOHYD 856 856 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 1166 1166 PALMITATE (BY SIMILARITY).
FT CONFLICT 206 206 G -> A (IN REF. 2).
FT CONFLICT 925 926 RR -> PG (IN REF. 2).
FT CONFLICT 1018 1018 M -> I (IN REF. 2).
FT CONFLICT 1156 1156 M -> I (IN REF. 2).
SQ SEQUENCE 1234 AA; 136635 MW; FAB4ED12BB916216 CRC64;

Query Match 60.4%; Score 58; DB 1; Length 1234;
Best Local Similarity 63.2%; Pred. No. 0.35;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 2 KASTPGAAQIQEVKEQRI 20
    || || | | | | | | | |
Db 1066 KAVAPGDKPKIQEVKEQRV 1084

RESULT 6
B3A2_MOUSE ID B3A2_MOUSE STANDARD; PRT; 1237 AA.
AC P13808; Q9ES09; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
GN SLC4A2 OR AE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=89034212; PubMed=3182834;
RA Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
RT "Cloning and characterization of a murine band 3-related cDNA from
RL kidney and from a lymphoid cell line.";
RN [2]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RX MEDLINE=20462926; PubMed=11006093;
RA Lecanda J., Uratsun K., Medina J.F.;
RT "Molecular cloning and genomic organization of the mouse AE2 anion
RL exchanger gene.";
RL Biochem. Biophys. Res. Commun. 276:117-124(2000).
CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=5;
CC Name=A;
CC IsoId=P13808-1; Sequence=Displayed;

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FT TRANSMEM 1159 1195 POTENTIAL.
FT DOMAIN 5 316 PRO-RICH.
FT DOMAIN 74 88 HIS-RICH.
FT CARBOHYD 855 855 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 864 864 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1169 1169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 1237 AA; 136535 MW; 2811D11051552BB2 CRC64;
SQ SEQUENCE 1237 AA; 136535 MW; 2811D11051552BB2 CRC64;

Query Match 60.4%; Score 58; DB 1; Length 1237;
Best Local Similarity 63.2%; Pred. No. 0.35;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KASTPGAAQIQEVKEQRI 20
  || || :|||||:
Db 1069 KAVAPGDKPKIQEVKEQV 1087

RESULT 8
B3A2_CAVPO STANDARD; PRT; 1238 AA.
AC Q920S8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2
DE anion exchanger).
DS SLC4A2 OR AE2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NH 2; TISSUE=Organ of Corti;
RX MEDLINE=9902378; PubMed=9804866;
RA Mhatre A.N., Charachon G., Alper A.L., Lalwani A.K.;
RT "The guinea pig cochlear AE2 anion exchanger: cDNA cloning and in situ
RT localization within the cochlea."
RL Biochim. Biophys. Acta 1414:1-15(1998).
CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
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CC -----
DR EMBL; AF121253; AAD19700.1; -
DR HSPR; P02730; IRTQ.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Lipoprotein; Palmitate.
FT DOMAIN 1 704 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 705 1238 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 705 728 POTENTIAL.
FT TRANSMEM 734 771 POTENTIAL.
FT TRANSMEM 791 813 POTENTIAL.
FT TRANSMEM 823 844 POTENTIAL.
FT TRANSMEM 845 897 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 898 915 POTENTIAL.
FT DOMAIN 916 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 931 951 POTENTIAL.
FT TRANSMEM 985 1007 POTENTIAL.
FT TRANSMEM 1033 1054 POTENTIAL.
FT TRANSMEM 1088 1133 POTENTIAL.
FT TRANSMEM 1160 1196 POTENTIAL.
FT DOMAIN 5 316 PRO-RICH.
FT DOMAIN 74 88 HIS-RICH.
FT CARBOHYD 856 856 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 865 865 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 879 879 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 1170 1170 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 1238 AA; 137358 MW; FAI739862ED5ADBFCRC64;

Query Match 60.4%; Score 58; DB 1; Length 1238;
Best Local Similarity 63.2%; Pred. No. 0.35;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KASTPGAAQIQEVKEQRI 20
  || || :|||||:
Db 1070 KAVAPGDKPKIQEVKEQV 1088

RESULT 9
B3A2_HUMAN STANDARD; PRT; 1241 AA.
AC P04920; Q969L3;
DT 13-AUG-1987 (Rel. 05, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
DS SLC4A2 OR AE2 OR EPB3L1 OR HKB3 OR MPB3L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=92223115; PubMed=1562608;
RA Gehrig H., Mueller W., Appelhans H.;
RT "Complete nucleotide sequence of band 3 related anion transport
RT protein AE2 from human kidney."
RL Biochim. Biophys. Acta 1130:326-328(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carinici P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 375-1241 FROM N.A.
RX MEDLINE=86274622; PubMed=3015590;
RA Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
RA Cioe L., Roversa G., Curtis P.J.;
RT "Cloning and structural characterization of a human non-erythroid
RT band 3-like protein."

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RL EMBO J. 5:1205-1214(1986).
CC -1- DISTRIBUTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms seem to exist;
CC Name=A;
CC IsoId=P04920-1; Sequence=Displayed;
CC Name=B1;
CC IsoId=P04920-2; Sequence=VSP_000456;
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
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CC EMBL; X62137; CAA44067.1; -
CC EMBL; BC009386; AAH09386.1; -
CC EMBL; BC009434; AAH09434.1; -
CC EMBL; X03918; CAA27556.1; -
CC PIR; S21086; S21086.
CC HSSP; P02730; IBTQ.
CC Genew; HGNC:11028; SLC4A2.
CC MIM; 109280; -
CC GO; GO:0005624; C:membrane fraction; TAS.
CC GO; GO:0008509; F:anion transporter activity; TAS.
CC GO; GO:0006820; P:anion transport; TAS.
CC InterPro; IPR001717; Anion_exchange.
CC InterPro; IPR003020; HCO3_cotransp.
CC Pfam; PF00955; HCO3_cotransp; 1.
CC PRINTS; PR01231; HCO3TRNSPORT.
CC TIGRams; TIGR00834; ae; 1.
CC PROSITE; PS00219; ANION_EXCHANGER_1; 1.
CC PROSITE; PS00220; ANION_EXCHANGER_2; 1.
CC Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
CC Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
CC DOMAIN 1 707 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 708 1241 MEMBRANE (ANION EXCHANGE).
CC TRANSMEM 708 731 POTENTIAL.
CC TRANSMEM 737 774 POTENTIAL.
CC TRANSMEM 784 816 POTENTIAL.
CC TRANSMEM 826 847 POTENTIAL.
CC DOMAIN 848 900 EXOPLASMIC LOOP (POTENTIAL).
CC TRANSMEM 901 918 POTENTIAL.
CC DOMAIN 919 933 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 934 954 POTENTIAL.
CC TRANSMEM 988 1010 POTENTIAL.
CC TRANSMEM 1036 1059 POTENTIAL.
CC TRANSMEM 1091 1135 POTENTIAL.
CC TRANSMEM 1163 1199 POTENTIAL.
CC DOMAIN 5 320 PRO-RICH.
CC CARBOHYD 859 859 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 868 868 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 882 882 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC LIPID 1173 1173 PALMITATE (BY SIMILARITY).
CC VARSPIC 1 17 MSSAPRLPAKGSDFCT -> MTQ (in isoform B1).
CC /FtId=VSP_000456.
CC CONFLICT 68 68 E -> M (IN REF. 1).
CC CONFLICT 74 74 H -> R (IN REF. 1).
CC CONFLICT 92 92 D -> G (IN REF. 1).
CC CONFLICT 122 122 E -> V (IN REF. 1).
CC CONFLICT 157 157 Q -> R (IN REF. 1).
CC CONFLICT 248 248 E -> R (IN REF. 1).
CC CONFLICT 399 399 MISSING (IN REF. 3).
CC CONFLICT 447 447 L -> V (IN REF. 1).
CC CONFLICT 475 475 LLGHGHOAGAESDPHVTPEPLMGVPE -> CWGITMVRGLR
CC VTPSPSLSWFELR (IN REF. 3).
CC CONFLICT 485 486 EL -> DV (IN REF. 1 AND 3).
FT CONFLICT 666 681 AAGAAEDDPIRRTGRP -> RQGLKMIKPSADGAA (IN
FT REF. 1 AND 3).
FT CONFLICT 824 824 Q -> R (IN REF. 1 AND 3).
FT CONFLICT 902 902 L -> P (IN REF. 1 AND 3).
SQ SEQUENCE 1241 AA; 136966 MW; B116908C5A71DB77 CRC64;
Query Match 60.4%; Score 58; DB 1; Length 1241;
Best Local Similarity 63.2%; Pred. No. 0.35;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 2 KASTPGAAAOIQEVKEORI 20
DB 1073 KAVAPGDKPIQEVKEQRV 1091
RESULT 10
B3A3_MOUSE
ID B3A3_MOUSE STANDARD; PRT; 1227 AA.
AC P16283;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 3 (Neuronal band 3-like protein).
GN SIC4A3 OR AE3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90075236; PubMed=2686841;
RA Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,
RA Schneider K.;
RT "Regulation of intracellular pH by a neuronal homolog of the
RT erythrocyte anion exchanger.";
RL Cell 59:927-937(1989).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=94171936; PubMed=8126106;
RA Morgans C.W., Kopito R.R.;
RT "Generation of truncated brain AE3 isoforms by alternate mRNA
RT processing.";
RL J. Cell Sci. 106:1275-1282(1993).
CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=FL-AE3;
CC IsoId=P16283-1; Sequence=Displayed;
CC Name=J11-AE3;
CC IsoId=P16283-2; Sequence=VSP_000464, VSP_000465;
CC Name=14-AE3;
CC IsoId=P16283-3; Sequence=VSP_000466, VSP_000467;
CC -1- TISSUE SPECIFICITY: NEURONAL.
CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
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CC EMBL; M28383; AAA37184.1; -
CC EMBL; S69314; AAB30140.1; -
CC PIR; A36368; A36368.
CC HSSP; P02730; IBTQ.
CC MGD; MGI:109350; Slc4a3.
CC InterPro; IPR001717; Anion_exchange.
CC InterPro; IPR003020; HCO3_cotransp.
CC Pfam; PF00955; HCO3_cotransp; 1.
CC PRINTS; PR01231; HCO3TRNSPORT.

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DR TIGRFAMS; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 707
FT DOMAIN 708 1227 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 708 1227
FT TRANSMEM 736 773 POTENTIAL.
FT TRANSMEM 793 815 POTENTIAL.
FT TRANSMEM 825 846 POTENTIAL.
FT TRANSMEM 888 905 POTENTIAL.
FT TRANSMEM 921 941 POTENTIAL.
FT TRANSMEM 975 997 POTENTIAL.
FT TRANSMEM 1023 1044 POTENTIAL.
FT TRANSMEM 1078 1123 POTENTIAL.
FT TRANSMEM 1150 1186 POTENTIAL.
FT DOMAIN 135 145 POLY-GLU.
FT CARBOHYD 868 868 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 1160 1160 PALMITATE (BY SIMILARITY).
FT VARSPLIC 381 391 AALLDLEQTL -> RAFWAGNESLL (in isoform 311-AE3).
FT /FTID-VSP_000464.
FT VARSPLIC 392 1227 Missing (in isoform 311-AE3).
FT /FTID-VSP_000465.
FT VARSPLIC 487 503 KPLHMPGGDGHGKSLK -> FCVLRSPSPCLGETVTEGKA
FT (in isoform 14-AE3).
FT /FTID-VSP_000466.
FT VARSPLIC 504 1227 Missing (in isoform 14-AE3).
FT /FTID-VSP_000467.
FT SEQUENCE 1227 AA; 135164 MW; D5BEC46E03F4251C CRC64;
Query Match 56.2%; Score 54; DB 1; Length 1227;
Best Local Similarity 61.1%; Pred. No. 1.5;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 3 ASTPGAAAIQIEVKQRI 20
DB 1061 AIAPGDKPQIEVREQRV 1078
RESULT 11
B3A3_RAT
ID B3A3_RAT STANDARD; PRT; 1227 AA.
AC P23348.
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 3 (Neuronal band 3-like protein).
GN SLC4A3 OR AE3 OR B3RP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90094439; PubMed=2294114;
RA Kudrycki K.E., Newman P.R., Shull G.E.;
RT "CDNA cloning and tissue distribution of mRNAs for two proteins that
are related to the band 3 Cl-/HCO3-exchanger.";
RL J. Biol. Chem. 265:462-471(1990).
CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: NEURONAL.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC -----
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CC EMBL; J05167; AAA40798.1; -.
CC PIR; B34911; B34911.
DR HSSP; P02730; LBQ.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMS; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Lipoprotein; Palmitate.
FT DOMAIN 1 707 CYTOPLASMIC.
FT DOMAIN 708 1227 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 708 1227
FT TRANSMEM 736 773 POTENTIAL.
FT TRANSMEM 793 815 POTENTIAL.
FT TRANSMEM 825 846 POTENTIAL.
FT TRANSMEM 888 905 POTENTIAL.
FT TRANSMEM 906 920 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 921 941 POTENTIAL.
FT TRANSMEM 975 997 POTENTIAL.
FT TRANSMEM 1023 1044 POTENTIAL.
FT TRANSMEM 1078 1123 POTENTIAL.
FT TRANSMEM 1150 1186 POTENTIAL.
FT CARBOHYD 868 868 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 1160 1160 PALMITATE (BY SIMILARITY).
FT DOMAIN 135 145 HIS-RICH.
FT DOMAIN 155 161 POLY-GLU.
FT DOMAIN 307 312 POLY-PRO.
FT DOMAIN 307 312 POLY-LYS.
FT DOMAIN 441 444 POLY-SER.
FT DOMAIN 1179 1182 POLY-LEU.
FT SEQUENCE 1227 AA; 135406 MW; 3EB1620EE011730E CRC64;
Query Match 56.2%; Score 54; DB 1; Length 1227;
Best Local Similarity 61.1%; Pred. No. 1.5;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 3 ASTPGAAAIQIEVKQRI 20
DB 1061 AIAPGDKPQIEVREQRV 1078
RESULT 12
B3A3_HUMAN
ID B3A3_HUMAN STANDARD; PRT; 1232 AA.
AC P48751.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain
DE band 3-like protein) (CAE3/BAE3).
DE SLC4A3 OR AE3.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BAE3).
RC TISSUE=Heart;
RX MEDLINE=95008042; PubMed=7923606;
RA Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,
RA Alper S.L.;
RT "Molecular cloning, expression, and chromosomal localization of two
RT isoforms of the AE3 anion exchanger from human heart.";
RL Circ. Res. 75:603-614(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM CAE3).
RC TISSUE=Heart;
RA Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;

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Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-) EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT CL(-).  
 -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 -1- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=2;  
 Comment=Additional isoforms seem to exist;  
 Name=BAE3;  
 IsoId=P48751-1; Sequence=Displayed;  
 Name=CAE3;  
 IsoId=P48751-2; Sequence=VSP\_000462, VSP\_000463;  
 -1- TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING VENTRICLE.  
 -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
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 EMBL; U05596; AAA50748.1; -;  
 EMBL; L27213; AAB05850.1; -;  
 PIR; I38496; I38496.  
 HSP; P02730; IRTQ.  
 Genew; HGNC:11029; SLC4A3.  
 MIM; 106195; -;  
 GO; GO:0005887; C: integral to plasma membrane; TAS.  
 GO; GO:0005624; C: membrane fraction; TAS.  
 GO; GO:0005452; F: inorganic anion exchanger activity; TAS.  
 GO; GO:0006832; P: small molecule transport; TAS.  
 InterPro; IPR001717; Anion-exchange.  
 InterPro; IPR003020; HCO3\_cotranspt.  
 Pfam; PF00955; HCO3\_cotransp; 1.  
 PRINTS; PR01231; HCO3TRNSPORT.  
 TIGRFAMS; TIGR00834; ae; 1.  
 PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 Transmembrane; Glycoprotein; Palmitate; Antiport; Ion transport;  
 Anion exchange; Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 708 CYTOPLASMIC.  
 FT DOMAIN 709 1232 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 709 731 POTENTIAL.  
 FT TRANSMEM 731 774 POTENTIAL.  
 FT TRANSMEM 794 816 POTENTIAL.  
 FT TRANSMEM 826 847 POTENTIAL.  
 FT TRANSMEM 893 910 POTENTIAL.  
 FT DOMAIN 911 925 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 926 946 POTENTIAL.  
 FT TRANSMEM 980 1002 POTENTIAL.  
 FT TRANSMEM 1028 1049 POTENTIAL.  
 FT TRANSMEM 1083 1128 POTENTIAL.  
 FT TRANSMEM 1155 1191 POTENTIAL.  
 FT DOMAIN 136 149 POLY-GLU.  
 FT DOMAIN 152 161 PRO-RICH.  
 FT DOMAIN 202 207 POLY-SER.  
 FT DOMAIN 308 313 POLY-LYS.  
 FT DOMAIN 442 445 POLY-SER.  
 FT DOMAIN 1184 1187 POLY-LEU.  
 FT LIPID 1165 1165 PALMITATE (BY SIMILARITY).  
 FT VARSPLIC 1 296 Missing (in isoform CAE3).  
 FT VARSPLIC 297 299 /FTid-VSP\_000462.  
 FT VARSPLIC 297 299 SPS -> MPA (in isoform CAE3).  
 FT VARSPLIC 297 299 /FTid-VSP\_000463.  
 FT CONFLICT 304 304 I -> V (IN REF. 2).  
 FT CONFLICT 343 343 R -> P (IN REF. 2).  
 FT CONFLICT 466 466 P -> S (IN REF. 2).  
 FT CONFLICT 608 608 S -> G (IN REF. 2).  
 FT CONFLICT 702 702 D -> A (IN REF. 2).

FT CONFLICT 812 813 GS -> FI (IN REF. 2).  
 FT CONFLICT 822 822 F -> L (IN REF. 2).  
 FT CONFLICT 861 861 A -> S (IN REF. 2).  
 FT CONFLICT 867 867 EGSIA -> D (IN REF. 2).  
 FT CONFLICT 875 875 S -> C (IN REF. 2).  
 FT CONFLICT 885 885 S -> G (IN REF. 2).  
 FT CONFLICT 887 887 R -> E (IN REF. 2).  
 FT CONFLICT 899 899 L -> P (IN REF. 2).  
 FT CONFLICT 1096 1096 I -> M (IN REF. 2).  
 SQ SEQUENCE 1232 AA; 135706 MW; 1825BE15977C3821 CRC64;  
 Query Match 56.2%; Score 54; DB 1; Length 1232;  
 Best Local Similarity 61.1%; Pred. No. 1.5;  
 Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 ASTPGAAAOIQEVKEORI 20  
 Db 1066 AIAPGKPKQIQEVKEQRV 1083  
 RESULT 13  
 B3A3 RABIT  
 ID B3A3 RABIT STANDARD; PRT; 1233 AA.  
 AC Q18917;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Anion exchange protein 3 (Neuronal band 3-like protein) (Anion  
 DE exchanger 3 brain isoform).  
 GN SLC4A3 OR AE3.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Abuladze N., Pushkin A., Kurtz I.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: NEURONAL.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF031650; AAB86859.1; -;  
 DR HSP; P02730; IRTQ.  
 DR InterPro; IPR001717; Anion-exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 KW Anion exchange; Lipoprotein; Palmitate.  
 FT DOMAIN 1 709 CYTOPLASMIC.  
 FT DOMAIN 710 1233 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 710 732 POTENTIAL.  
 FT TRANSMEM 738 775 POTENTIAL.  
 FT TRANSMEM 795 817 POTENTIAL.  
 FT TRANSMEM 827 848 POTENTIAL.  
 FT TRANSMEM 894 911 POTENTIAL.  
 FT DOMAIN 912 926 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 927 947 POTENTIAL.  
 FT TRANSMEM 981 1003 POTENTIAL.

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FT TRANSEM 1029 1050 POTENTIAL.
FT TRANSEM 1084 1129 POTENTIAL.
FT TRANSEM 1156 1192 POTENTIAL.
FT CARBOHYD 874 874 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 1166 1166 PALMITATE (BY SIMILARITY).
FT DOMAIN 74 83 HIS-RICH.
FT DOMAIN 136 150 POLY-GLU.
FT DOMAIN 203 208 POLY-SER.
FT DOMAIN 309 312 POLY-LYS.
FT DOMAIN 443 446 POLY-SER.
FT DOMAIN 1185 1188 POLY-LEU.
FT SEQUENCE 1233 AA; 135759 MW; AE486423B9818583 CRC64;

Query Match 56.2%; Score 54; DB 1; Length 1233;
Best Local Similarity 61.1%; Pred. No. 1.5;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 ASTPGAAAOIQEVKEQRI 20
| || |||||:|:|:|
Db 1067 AIAPGDKPQIQEVREQRV 1084

RESULT 14
RRPP_MUMPE STANDARD; PRT; 391 AA.
AC P16072;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase alpha subunit (EC 2.7.7.48) (Nucleocapsid
DE phosphoprotein).
GN P.
OS Mumps virus (strain Enders).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OC NCBI_TaxID=11167;
RX MEDLINE=88299965; Pubmed=3404121;
RA Takeuchi K., Hishiyama M., Yamada A., Sugiyama A.;
RT "Molecular cloning and sequence analysis of the mumps virus gene
RT encoding the P protein: mumps virus P gene is monocistronic.";
RL J. Gen. Virol. 69:2043-2049(1988).
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; D00351; BAA00259.1; -
CC PIR; JU0067; RNNZYA.
CC InterPro; IPR004897; Paramyx_P_V.
CC Pfam; PF03210; Paramyx_P_V; 1.
CC Transferrase; RNA-directed RNA polymerase; Nucleocapsid;
CC Phosphorylation.
CC SEQUENCE 391 AA; 41650 MW; 2802A11A5542B7A5 CRC64;

Query Match 46.9%; Score 45; DB 1; Length 391;
Best Local Similarity 52.6%; Pred. No. 12;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 KASTPGAAAOIQEVKEQRI 20
| ||||| |::|:|
Db 153 KRGGPAAAOQQTQIEEGI 171

Search completed: September 3, 2003, 11:46:57
Job time : 10.25 secs
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RESULT 15
RRPP_MUMPM STANDARD; PRT; 391 AA.
AC P16595;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase alpha subunit (EC 2.7.7.48) (Nucleocapsid
DE phosphoprotein).
GN P.
OS Mumps virus (strain Miyahara vaccine).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OC NCBI_TaxID=11171;
RX MEDLINE=88299965; Pubmed=3404121;
RA Takeuchi K., Hishiyama M., Yamada A., Sugiyama A.;
RT "Molecular cloning and sequence analysis of the mumps virus gene
RT encoding the P protein: mumps virus P gene is monocistronic.";
RL J. Gen. Virol. 69:2043-2049(1988).
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D00352; BAA00260.1; -
CC PIR; JU0066; RNNZYA.
CC InterPro; IPR004897; Paramyx_P_V.
CC Pfam; PF03210; Paramyx_P_V; 1.
CC Transferrase; RNA-directed RNA polymerase; Nucleocapsid;
CC Phosphorylation.
CC SEQUENCE 391 AA; 41587 MW; FD7053C9C7BC522C CRC64;

Query Match 46.9%; Score 45; DB 1; Length 391;
Best Local Similarity 52.6%; Pred. No. 12;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 KASTPGAAAOIQEVKEQRI 20
| ||||| |::|:|
Db 153 KRGGPAAAOQQTQIEEGI 171

Search completed: September 3, 2003, 11:46:57
Job time : 10.25 secs
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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	112	100.0	911	1	B3AT_HUMAN	P02730	homo sapien
2	108	96.4	927	1	B3AT_RAT	P23562	rattus norv
3	108	96.4	929	1	B3AT_MOUSE	P04919	mus musculus
4	82	73.2	922	1	B3AT_CHICK	P05575	gallus gall
5	74	66.1	1234	1	B3A2_RAT	P23347	rattus norv
6	74	66.1	1237	1	B3A2_MOUSE	P13808	mus musculus
7	74	66.1	1237	1	B3A2_RABIT	P48746	oryctolagus
8	74	66.1	1241	1	B3A2_HUMAN	P04920	homo sapien
9	73	65.2	1238	1	B3A2_CAVPO	Q920S8	cavia porce
10	68	60.7	1227	1	B3A3_MOUSE	P16283	mus musculus
11	68	60.7	1227	1	B3A3_RAT	P23348	rattus norv
12	62	55.4	1232	1	B3A3_HUMAN	P48751	homo sapien
13	62	55.4	1233	1	B3A3_RABIT	O18917	oryctolagus
14	58	51.8	440	1	SOCT_HUMAN	Q8wxh5	homo sapien
15	52	46.4	336	1	LEGC_HUMAN	O96dt0	homo sapien
16	50	44.6	436	1	SOCT_MOUSE	Q91za6	mus musculus
17	50	44.6	918	1	B3AT_ONCMY	P32847	oncorhynch
18	49	43.8	336	1	UL16_EBV	P03221	epstein-bar
19	49	43.8	469	1	PPAF_ARATH	Q38924	arabidopsis
20	48	42.9	403	1	STAL_MOUSE	Q64685	mus musculus
21	47.5	42.4	304	1	WBP1_MOUSE	P97764	mus musculus
22	47	42.0	168	1	CYNS_ORYSA	O9fwk4	oryza sativ
23	47	42.0	234	1	YB46_METHH	O27214	methanobact
24	46	41.1	218	1	VNS3_AHSV1	Q64903	afrikan hor
25	46	41.1	218	1	VNS3_AHSV2	Q64914	afrikan hor
26	46	41.1	218	1	VNS3_AHSV8	Q64905	afrikan hor
27	46	41.1	578	1	HPCL_HUMAN	Q9uj83	homo sapien
28	45	40.2	403	1	SLA1_RAT	P13721	rattus norv
29	45	40.2	406	1	STA1_HUMAN	P15907	homo sapien
30	45	40.2	434	1	NO75_LUPLU	Q08841	lupinus lut
31	45	40.2	588	1	DNLI_THEVO	Q979a1	thermoplasm
32	45	40.2	859	1	DNK3B_MOUSE	O88509	mus musculus
33	44	39.3	179	1	Y458_ANASP	P29712	anabaena sp

sequence, conformation and a possible molecular mechanism for anion exchange.";  
 RL Biochem. J. 213:577-586(1983).  
 [7]  
 RP SEQUENCE OF 834-911.  
 RP MEDLINE=88228050; PubMed=3372523;  
 RA Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.;  
 "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein.";  
 RL J. Biol. Chem. 263:8232-8238(1988).  
 [8]  
 RP ROLE OF GLU-681, AND SEQUENCE OF 665-688.  
 RP MEDLINE=92332495; PubMed=1352774;  
 RA Jennings M.L., Smith J.S.;  
 "Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681.";  
 RL J. Biol. Chem. 267:13964-13971(1992).  
 [9]  
 RP PALMITOYLATION OF CYS-843.  
 RP MEDLINE=91358422; PubMed=1885574;  
 RA Okubo K., Hamasaki N., Hara K., Kageura M.;  
 "Palmitoylation of cysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-ILCLAVL found in band 3 protein and G2 protein of Rift Valley fever virus.";  
 RL J. Biol. Chem. 266:16420-16424(1991).  
 [10]  
 RP PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.  
 RP MEDLINE=20400020; PubMed=10942405;  
 RA Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E., Pinna L.A., Donella-Deana A.;  
 "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites.";  
 RL Blood 96:1550-1557(2000).  
 [11]  
 RP VARIANT MEMPHIS GLU-56.  
 RP MEDLINE=91329825; PubMed=1678289;  
 RA Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delaunay J., Wajcman H., Bursaux E.;  
 "Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the structural modification (Lys 56-->Glu) by protein chemistry methods.";  
 RL Blood 78:1117-1120(1991).  
 [12]  
 RP VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.  
 RP MEDLINE=92107882; PubMed=1722314;  
 RA Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T., Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;  
 "Deletion in erythrocyte band 3 gene in malaria-resistant Southeast Asian ovalocytosis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).  
 [13]  
 RP VARIANT HS ARG-327.  
 RP MEDLINE=92329950; PubMed=1378323;  
 RA Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C., Cohen C.M.;  
 "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2.";  
 RL Blood 80:523-529(1992).  
 [14]  
 RP VARIANT HE 400-ALA--ALA-408 DEL.  
 RP MEDLINE=92167271; PubMed=1538405;  
 RA Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M., Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M., Gratzel W.B.;  
 "Basis of unique red cell membrane properties in hereditary ovalocytosis.";  
 RL J. Mol. Biol. 223:949-958(1992).  
 [15]  
 RP VARIANT HS LEU-868.  
 RP MEDLINE=93343855; PubMed=8343110;

RA Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;  
 "Band 3 HP, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3.";  
 RL Biochem. J. 293:317-320(1993).  
 [16]  
 RP VARIANT MONTEFIORE LYS-40.  
 RP MEDLINE=93229758; PubMed=8471774;  
 RA Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L., Schwartz R.S.;  
 "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore).";  
 RL Blood 81:2155-2165(1993).  
 [17]  
 RP VARIANT BLOOD GROUP DI(A)(MEMPHIS-II.  
 RP MEDLINE=94266802; PubMed=8206915;  
 RA Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;  
 "Band 3 Memphis variant II. Altered stilbene disulfonate binding and the Diego (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation Pro-854-->Leu.";  
 RL J. Biol. Chem. 269:16155-16158(1994).  
 [18]  
 RP VARIANT BLOOD GROUP WR(A).  
 RP MEDLINE=95111140; PubMed=7812009;  
 RA Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S., Tanner M.J.;  
 "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain conditions.";  
 RL Blood 85:541-547(1995).  
 [19]  
 RP VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.  
 RP MEDLINE=95134893; PubMed=7530501;  
 RA Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S., Alper S.L., Brugnara C., Wichterle H., Palek J.;  
 "Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis.";  
 RL Blood 85:634-640(1995).  
 [20]  
 RP VARIANT HS ASP-771.  
 RP MEDLINE=96136073; PubMed=8547122;  
 RA Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P., Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;  
 "Band 3 Chur: a variant associated with band 3-deficient hereditary spherocytosis and substitution in a highly conserved position of transmembrane segment 11.";  
 RL Br. J. Haematol. 91:804-810(1995).  
 [21]  
 RP VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.  
 RP MEDLINE=97099297; PubMed=8943874;  
 RA Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V., Palek J.;  
 "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency.";  
 RL Blood 88:4366-4374(1996).  
 [22]  
 RP VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.  
 RP MEDLINE=96225450; PubMed=8640229;  
 RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T., Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A., Gallacher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 "Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";  
 RL Nat. Genet. 13:214-218(1996).  
 [23]  
 RP VARIANTS HS SER-147 AND MET-488.  
 RP MEDLINE=97351102; PubMed=9207478;  
 RA Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Boron M., Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,

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Query Match      100.0%; Score 112; DB 1; Length 911;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDVPYVK 20
    |||||
Db 807 DRILLFKPKYHPDVPYVK 826

RESULT 2
BJAT_RAT
ID BJAT_RAT STANDARD; PRT; 927 AA.
AC P23562;
DT 01-NOV-1991 (Rel. 20, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
GN SLC4A1 OR AEL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 46-927 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=89255254; PubMed=2722777;
RA Kudrycki K.E., Shull G.E.;
RT "Primary structure of the rat kidney band 3 anion exchange protein
deduced from a cDNA.";
RL J. Biol. Chem. 264:8185-8192(1989).
RN [2]
RP SEQUENCE OF 1-45 FROM N.A.
RA Kudrycki K.E., Shull G.E.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
CC MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
CC WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
CC CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).
CC -!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
CC AND APPEARS TO BE TETRAMERIC.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
CC BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
CC COLLECTING DUCTS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Erythrocyte;
CC IsoId=P23562-1; Sequence=Displayed;
CC Name=Kidney;
CC IsoId=P23562-2; Sequence=VSP_000455;
CC -!- TISSUE SPECIFICITY: Kidney.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04793; AAA40800.1; ALT_INIT.
DR EMBL; L02943; AAA40801.1;
DR PIR; A33810; A33810.
DR HSP; P02730; 1BTS.
DR InterPro; IPR001717; Anion_exchanger.
DR InterPro; IPR003020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;

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KW Lipoprotein; Palmitate; Alternative splicing.
FT DOMAIN 1 420 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 421 927 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 421 441 POTENTIAL.
FT TRANSMEM 454 473 POTENTIAL.
FT TRANSMEM 477 496 POTENTIAL.
FT TRANSMEM 508 527 POTENTIAL.
FT TRANSMEM 540 558 POTENTIAL.
FT DOMAIN 559 585 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 585 604 POTENTIAL.
FT DOMAIN 605 619 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 620 640 POTENTIAL.
FT DOMAIN 641 676 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 677 696 POTENTIAL.
FT TRANSMEM 715 735 POTENTIAL.
FT TRANSMEM 779 796 POTENTIAL.
FT TRANSMEM 801 822 POTENTIAL.
FT TRANSMEM 860 881 POTENTIAL.
FT CARBOHYD 658 658 N-LINKED (GLCNAC...) (PROBABLE).
FT LIPID 859 859 PALMITATE (BY SIMILARITY).
FT VARSPPLIC 1 79 Missing (in isoform Kidney).
SQ SEQUENCE 927 AA; 103172 MW; 681A228474E5E9DE CRC64;

Query Match      96.4%; Score 108; DB 1; Length 927;
Best Local Similarity 95.0%; Pred. No. 1.3e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDVPYVK 20
    |||||
Db 823 DRILLFKPKYHPDVPYVK 842

RESULT 3
BJAT_MOUSE
ID BJAT_MOUSE STANDARD; PRT; 929 AA.
AC P04919;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
DE (MEB3).
GN SLC4A1 OR AEL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85268011; PubMed=2410791;
RA Kopito R.R., Lodish H.F.;
RT "Primary structure and transmembrane orientation of the murine anion
exchange protein.";
RL Nature 316:234-238(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86034211; PubMed=3840489;
RA Kopito R.R., Lodish H.F.;
RT "Structure of the murine anion exchange protein.";
RL J. Cell. Biochem. 29:1-17(1985).
RN [3]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=87250387; PubMed=3036795;
RA Kopito R.R., Andersson M., Lodish H.F.;
RT "Structure and organization of the murine band 3 gene.";
RL J. Biol. Chem. 262:8035-8040(1987).
RN [4]
RP SEQUENCE FROM N.A.
RA Kopito R.R.;
RL Submitted (JUL-1987) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 11-929 FROM N.A.
RX MEDLINE=86274622; PubMed=3015590;

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Demuth D.R., Shove L.C., Ballantine M., Palumbo A., Fraser P.J.,  
 Cioe L., Roversa G., Curtis P.J.;  
 "Cloning and structural characterization of a human non-erythroid  
 band 3-like protein.";  
 RL EMBL J. 5:1205-1214(1986).  
 [6]  
 RP SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.  
 RX MEDLINE=89229233; PubMed=2713407;  
 RA Rada M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,  
 Passow H.;  
 "Major proteolytic fragments of the murine band 3 protein as obtained  
 after in situ proteolysis.";  
 RL Biochim. Biophys. Acta 980:291-298(1989).  
 CC -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE  
 ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS  
 INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS  
 THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING  
 SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND  
 HEMOGLOBIN.  
 CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 AND APPEARS TO BE TETRAMERIC.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=2;  
 Name=Erythrocyte;  
 CC IsoId=P04919-1; Sequence=Displayed;  
 CC Name=Kidney;  
 CC IsoId=P04919-2; Sequence=VSP\_000454;  
 CC -1- TISSUE SPECIFICITY: ERYTHROCYTE.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC  
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 DR EMBL; X02677; CAA26506.1; -;  
 DR EMBL; M29379; AAA37187.1; -;  
 DR EMBL; J02756; AAA37278.1; -;  
 DR EMBL; X03917; CAA27555.1; -;  
 DR PIR; A25314; A25314.  
 DR HSSP; P02730; 1BTS.  
 DR MGD; MGI:109393; Slc4a1.  
 DR InterPro; IPR001717; Anion\_exchanger.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;  
 Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 422  
 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 423 929  
 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 423 443  
 POTENTIAL.  
 FT TRANSMEM 456 475  
 POTENTIAL.  
 FT TRANSMEM 479 498  
 POTENTIAL.  
 FT TRANSMEM 510 529  
 POTENTIAL.  
 FT TRANSMEM 542 560  
 POTENTIAL.  
 FT DOMAIN 561 586  
 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 587 606  
 POTENTIAL.  
 FT DOMAIN 607 621  
 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 622 642  
 POTENTIAL.  
 FT DOMAIN 643 678  
 EXOPLASMIC LOOP (POTENTIAL).  
 FT TRANSMEM 679 698  
 POTENTIAL.  
 FT TRANSMEM 717 737  
 POTENTIAL.  
 FT TRANSMEM 781 798  
 POTENTIAL.  
 FT TRANSMEM 803 824  
 POTENTIAL.  
 FT TRANSMEM 862 883  
 POTENTIAL.  
 FT CARBOHYD 660  
 N-LINKED (GLCNAC. . .) (PROBABLE).

FT LIPID 861 861 PALMITATE (BY SIMILARITY).  
 FT VARSPLIC 1 79 Missing (in isoform kidney).  
 FT FTId=VSP\_000454.  
 FT CONFLICT 467 467 G -> S (IN REF. 5).  
 SQ SEQUENCE 929 AA; 103135 MW; 5C0E281C394FB614 CRC64;  
 Query Match 96.4%; Score 108; DB 1; Length 929;  
 Best Local Similarity 95.0%; Pred. No. 1.3e-08;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRILLFKPKYHPDVPVK 20  
 DB 825 DRILLFKPKYHPDVPVK 844  
 RESULT 4  
 B3AT\_CHICK STANDARD; PRT; 922 AA.  
 ID B3AT\_CHICK  
 AC P15575;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Band 3 anion transport protein.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
 CC Gallus.  
 CC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89039870; PubMed=3185555;  
 RA Kim H.R.C., Yew N.S., Ansorge W., Voss H., Schwager C.,  
 Vennstroem B., Zenke M., Engel J.D.;  
 "Two different mRNAs are transcribed from a single genomic locus  
 encoding the chicken erythrocyte anion transport proteins (band 3).";  
 RL Mol. Cell. Biol. 8:4416-4424(1988).  
 CC -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE  
 ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS  
 INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS  
 THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING  
 SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND  
 HEMOGLOBIN.  
 CC -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY  
 AND APPEARS TO BE TETRAMERIC.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: ERYTHROCYTE.  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC  
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 -----  
 DR EMBL; M23404; AAA48753.1; -;  
 DR HSSP; P02730; 1BTS.  
 DR InterPro; IPR001717; Anion\_exchanger.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.  
 FT DOMAIN 1 416  
 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 417 922  
 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 417 437  
 POTENTIAL.  
 FT TRANSMEM 450 469  
 POTENTIAL.  
 FT TRANSMEM 473 492  
 POTENTIAL.  
 FT TRANSMEM 504 523  
 POTENTIAL.  
 FT TRANSMEM 536 554  
 POTENTIAL.



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FT DOMAIN          555 579 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM        580 599 POTENTIAL.
FT DOMAIN          600 614 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM        615 635 POTENTIAL.
FT DOMAIN          636 671 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM        672 691 POTENTIAL.
FT TRANSMEM        710 730 POTENTIAL.
FT TRANSMEM        774 791 POTENTIAL.
FT TRANSMEM        796 817 POTENTIAL.
FT TRANSMEM        855 876 POTENTIAL.
FT CARBOHYD        653 653 N-LINKED (GLCNAC... ) (PROBABLE).
SQ SEQUENCE        922 AA; 102223 MW; FF4ECAD6D60CF0CF CRC64;

Query Match          73.2%; Score 82; DB 1; Length 922;
Best Local Similarity 78.9%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRILLFPKPKYHPDVPYK 19
    ||||| ||||| |||
DB 818 DRILLLLMPKPKYHPKPYV 836

RESULT 5
B3A2_RAT
AC P23347; STANDARD; PRT; 1234 AA.
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
GN SLC4A2 OR AE2 OR B3RP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90094439; PubMed=2294114;
TX TISSUE=Stomach;
RA Kudrycki K.E., Newman P.R., Shull G.E.;
RT "cDNA cloning and tissue distribution of mRNAs for two proteins that
RN J. Biol. Chem. 265:462-471(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319095; PubMed=2371270;
RA Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
TX Kopito R.R.;
RT "Functional expression and subcellular localization of an anion
RL Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; J05166; AAA40799.1; -
DR PIR; A34911; A34911.
DR HSP; P02730; 1BTO.
DR InterPro; IPR001717; Anion_exchange.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.

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DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Lipoprotein; Palmitate.
FT DOMAIN          1 704 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM        705 1234 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM        705 728 POTENTIAL.
FT TRANSMEM        734 771 POTENTIAL.
FT TRANSMEM        791 813 POTENTIAL.
FT TRANSMEM        823 844 POTENTIAL.
FT DOMAIN          844 893 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM        894 911 POTENTIAL.
FT DOMAIN          912 926 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM        927 947 POTENTIAL.
FT TRANSMEM        981 1003 POTENTIAL.
FT TRANSMEM        1029 1050 POTENTIAL.
FT TRANSMEM        1084 1129 POTENTIAL.
FT TRANSMEM        1156 1192 POTENTIAL.
FT DOMAIN          5 317 PRO-RICH.
FT DOMAIN          74 88 HIS-RICH.
FT CARBOHYD        856 856 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD        866 866 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD        878 878 N-LINKED (GLCNAC... ) (POTENTIAL).
FT LIPID           1166 1166 PALMITATE (BY SIMILARITY).
FT CONFLICT        206 206 G -> A (IN REF. 2).
FT CONFLICT        925 926 RR -> PG (IN REF. 2).
FT CONFLICT        1018 1018 M -> I (IN REF. 2).
FT CONFLICT        1156 1156 M -> I (IN REF. 2).
SQ SEQUENCE        1234 AA; 136635 MW; FAB4ED12BB916216 CRC64;

Query Match          66.1%; Score 74; DB 1; Length 1234;
Best Local Similarity 65.0%; Pred. No. 0.0025;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRILLFPKPKYHPDVPYK 20
    :|: || |||: ||||| |||
DB 1130 ERLHLLMPKPKHHPDVTYK 1149

RESULT 6
B3A2_MOUSE
ID B3A2_MOUSE STANDARD; PRT; 1237 AA.
AC P13808; Q9ES09; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
GN SLC4A2 OR AE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=89034212; PubMed=3182834;
RA Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
RT "Cloning and characterization of a murine band 3-related cDNA from
RT kidney and from a lymphoid cell line."
RL J. Biol. Chem. 263:17092-17099(1988).
[2]
RP SEQUENCE FROM N.A.; ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RX MEDLINE=20462926; PubMed=11006093;
RA Lecanda J., Urtasun R., Medina J.F.;
RT "Molecular cloning and genomic organization of the mouse AE2 anion
RT exchanger gene."
RL Biochem. Biophys. Res. Commun. 276:117-124(2000).
CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=5;
CC Name=A;
CC IsoID=P13808-1; Sequence=Displayed;

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FT TRANSMEM 1159 1195 POTENTIAL.  
 FT DOMAIN 5 316 PRO-RICH.  
 FT DOMAIN 74 88 HIS-RICH.  
 FT CARBOHYD 855 855 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 864 864 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 1169 1169 PALMITATE (BY SIMILARITY).  
 SQ SEQUENCE 1237 AA; 136535 MW; 2811D11051552BB2 CRC64;  
 Query Match 66.1%; Score 74; DB 1; Length 1237;  
 Best Local Similarity 65.0%; Pred. No. 0.0025;  
 Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 DRILLFKPKYHPDVPYK 20  
 Db 1133 ERLHLLLPKPKHPDVPYK 1152  
 RESULT 8  
 B3A2\_HUMAN  
 ID B3A2\_HUMAN STANDARD; PRT; 1241 AA.  
 AC P04920; O969L3;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).  
 GN SLC4A2 OR AE2 OR EPB3L1 OR HKB3 OR MPB3L.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RX MEDLINE=92223115; PubMed=1562608;  
 RA Gehrig H., Mueller W., Appelhaus H.;  
 RT Complete nucleotide sequence of band 3 related anion transport  
 RT protein AE2 from human kidney.";  
 RL Biochim. Biophys. Acta 1130:326-328(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM B1).  
 RC TISSUE=Brain;  
 RX MEDLINE=22386257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heltan E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE OF 375-1241 FROM N.A.  
 RX MEDLINE=86274622; PubMed=3015590;  
 RA Demuth D.R., Shove L.C., Ballantine M., Palumbo A., Fraser P.J.,  
 RA Cioe L., Roversa G., Curtis P.J.;  
 RT Cloning and structural characterization of a human non-erythroid  
 RT band 3-like protein.";  
 RL EMBO J. 5:1205-1214(1986).  
 CC -1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE  
 CC DISTRIBUTION.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=A;  
 CC IsoId=P04920-1; Sequence=Displayed;  
 CC Name=B1;  
 CC IsoId=P04920-2; Sequence=VSP\_000456;  
 CC -1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; X62137; CAA44067.1; -;  
 CC EMBL; BC009386; AAH09386.1; -;  
 CC EMBL; BC009434; AAH09434.1; -;  
 CC EMBL; X03918; CAA27556.1; -;  
 CC PIR; S21086; S21086.  
 CC HSSP; P02730; 1BTO.  
 CC Genew; HGNC:11028; SLC4A2.  
 CC MIM; 109280; -;  
 CC GO; GO:0005624; C:membrane fraction; TAS.  
 CC GO; GO:0008509; F:anion transporter activity; TAS.  
 CC GO; GO:0006820; P:anion transport; TAS.  
 CC InterPro; IPR001717; Anion\_exchange.  
 CC InterPro; IPR003020; HCO3\_cotransp.  
 CC Pfam; PF00955; HCO3\_cotransp; 1.  
 CC PRINTS; PR01231; HCO3TRNSPORT.  
 CC TIGRFS; TIGR00834; ae; 1.  
 CC PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 CC PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 CC Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 CC Anion exchange; Lipoprotein; Palmitate; Alternative splicing.  
 CC CYTOPLASMIC (POTENTIAL).  
 CC DOMAIN 1 707 MEMBRANE (ANION EXCHANGE).  
 CC FT DOMAIN 708 1241 POTENTIAL.  
 CC FT TRANSMEM 708 731 POTENTIAL.  
 CC FT TRANSMEM 737 774 POTENTIAL.  
 CC FT TRANSMEM 784 816 POTENTIAL.  
 CC FT TRANSMEM 826 847 POTENTIAL.  
 CC FT DOMAIN 848 900 EXOPLASMIC LOOP (POTENTIAL).  
 CC FT TRANSMEM 901 918 POTENTIAL.  
 CC FT DOMAIN 919 933 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 934 954 POTENTIAL.  
 CC FT TRANSMEM 988 1010 POTENTIAL.  
 CC FT TRANSMEM 1036 1059 POTENTIAL.  
 CC FT TRANSMEM 1091 1136 POTENTIAL.  
 CC FT TRANSMEM 1163 1199 POTENTIAL.  
 CC FT DOMAIN 5 320 PRO-RICH.  
 CC FT CARBOHYD 859 859 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 868 868 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 882 882 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT LIPID 1173 1173 PALMITATE (BY SIMILARITY).  
 CC FT VARSPLIC 1 17 MSSAPRLPAKGAQSFT -> MTQ (in isoform B1).  
 CC FT /FTID=VSP\_000456.  
 CC FT E -> M (IN REF. 1).  
 CC FT H -> R (IN REF. 1).  
 CC FT D -> G (IN REF. 1).  
 CC FT E -> V (IN REF. 1).  
 CC FT Q -> R (IN REF. 1).  
 CC FT E -> R (IN REF. 1).  
 CC FT MISSING (IN REF. 3).  
 CC FT L -> V (IN REF. 1).  
 CC FT 475 LIGHHGQAEADPHVTEPLMGVPE -> CWGITWVRGLR  
 CC FT 485 EL -> DV (IN REF. 1 AND 3).  
 CC FT 666 RAGAEEDPRLRTGR -> ROGOLKMPISADGAA (IN  
 CC FT 681 REF. 1 AND 3).  
 CC FT 824 Q -> R (IN REF. 1 AND 3).  
 CC FT 902 L -> P (IN REF. 1 AND 3).  
 CC FT CONFLICT 902

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SQ SEQUENCE 1241 AA; 136966 MW; B116908C5A71DB77 CRC64;
Query Match 66.1%; Score 74; DB 1; Length 1241;
Best Local Similarity 65.0%; Pred. No. 0.0026;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDVPYVK 20
   :|: || |||:|||| |||
Db 1137 ERLHLLMPKHPDVTYVK 1156

RESULT 9
B3A2_CAVPO STANDARD; PRT; 1238 AA.
ID B3A2_CAVPO
AC Q9Z0S8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2
DE anion exchanger).
GN SLC4A2 OR AE2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NIH 2; TISSUE=Organ of Corti;
RX MEDLINE=99023787; PubMed=9804866;
RA Whatre A.N., Charachon G., Alper A.L., Lalwani A.K.;
RT "The guinea pig cochlear AE2 anion exchanger: cDNA cloning and in situ
RT localization within the cochlea.";
RL Biochim. Biophys. Acta 1414:1-15(1998).
CC -|- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
CC DISTRIBUTION.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC
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CC
CC EMBL; AF121253; AAD19700.1; -
CC HSSP; P02730; 1BTO.
CC InterPro; IPR001717; Anion-exchange.
CC InterPro; IPR003020; HCO3_cotransp.
CC Pfam; PF00955; HCO3_cotransp; 1.
CC PRINTS; PR01231; HCO3TRNSPORT.
CC TIGRFAMs; TIGR00834; ae; 1.
CC PROSITE; PS00219; ANION_EXCHANGER_1; 1.
CC PROSITE; PS00220; ANION_EXCHANGER_2; 1.
KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
KW Anion exchange; Lipoprotein; Palmitate.
FT DOMAIN 1 704 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 705 1238 MEMBRANE (ANION EXCHANGE).
FT TRANSMEM 705 728 POTENTIAL.
FT TRANSMEM 734 771 POTENTIAL.
FT TRANSMEM 791 813 POTENTIAL.
FT TRANSMEM 823 844 POTENTIAL.
FT TRANSMEM 845 897 EXOPLASMIC LOOP (POTENTIAL).
FT TRANSMEM 898 915 POTENTIAL.
FT DOMAIN 916 930 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 931 951 POTENTIAL.
FT TRANSMEM 985 1007 POTENTIAL.
FT TRANSMEM 1033 1054 POTENTIAL.
FT TRANSMEM 1088 1133 POTENTIAL.
FT TRANSMEM 1160 1196 POTENTIAL.
FT DOMAIN 5 316 PRO-RICH.
FT DOMAIN 74 88 HIS-RICH.

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FT CARBOHYD 856 856 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 865 865 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 879 879 N-LINKED (GLCNAC... ) (POTENTIAL).
FT LIPID 1170 1170 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 1238 AA; 137358 MW; FA1739862ED5ADBF CRC64;
Query Match 65.2%; Score 73; DB 1; Length 1238;
Best Local Similarity 65.0%; Pred. No. 0.0036;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRILLFKPKYHPDVPYVK 20
   :|: || |||:|||| |||
Db 1134 ERLHLLMPKHPDVTYVK 1153

RESULT 10
B3A3_MOUSE STANDARD; PRT; 1227 AA.
ID B3A3_MOUSE
AC P16283;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anion exchange protein 3 (Neuronal band 3-like protein).
GN SLC4A3 OR AE3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90075236; PubMed=2686841;
RA Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,
RA Schneider K.;
RT "Regulation of intracellular pH by a neuronal homolog of the
RT erythrocyte anion exchanger.";
RL Cell 59:927-937(1989).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=94171936; PubMed=8126106;
RA Morgans C.W., Kopito R.R.;
RT "Generation of truncated brain AE3 isoforms by alternate mRNA
RT processing.";
RL J. Cell Sci. 106:1275-1282(1993).
CC -|- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=FL-AE3;
CC IsoId=P16283-1; Sequence=Displayed;
CC Name=311-AE3;
CC IsoId=P16283-2; Sequence=VSP_000464, VSP_000465;
CC Name=14-AE3;
CC IsoId=P16283-3; Sequence=VSP_000466, VSP_000467;
CC -|- TISSUE SPECIFICITY: NEURONAL.
CC -|- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CC
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CC
CC EMBL; M28383; AAA37184.1; -
CC EMBL; S69314; AAB30140.1; -
CC HSSP; P02730; 1BTO.
CC MGD; MGI:109350; SLC4a3.
CC InterPro; IPR001717; Anion-exchange.
CC InterPro; IPR003020; HCO3_cotransp.
CC Pfam; PF00955; HCO3_cotransp; 1.
CC PRINTS; PR01231; HCO3TRNSPORT.

```

DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 DR Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 KW Anion exchange; Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 707 CYTOPLASMIC.  
 FT DOMAIN 708 1227 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 708 730 POTENTIAL.  
 FT TRANSMEM 736 773 POTENTIAL.  
 FT TRANSMEM 793 815 POTENTIAL.  
 FT TRANSMEM 825 846 POTENTIAL.  
 FT TRANSMEM 888 905 POTENTIAL.  
 FT TRANSMEM 906 920 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 921 941 POTENTIAL.  
 FT TRANSMEM 921 941 POTENTIAL.  
 FT TRANSMEM 975 997 POTENTIAL.  
 FT TRANSMEM 1023 1044 POTENTIAL.  
 FT TRANSMEM 1078 1123 POTENTIAL.  
 FT TRANSMEM 1150 1186 POTENTIAL.  
 FT DOMAIN 135 145 POLY-GLU.  
 FT CARBOHYD 868 868 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 1160 1160 PALMITATE (BY SIMILARITY).  
 FT VARSPLIC 381 391 AALLDLEQTL -> RAFWAGNESLL (in isoform 311-AE3).  
 FT /FTId-VSP\_000464.  
 FT VARSPLIC 392 1227 Missing (in isoform 311-AE3).  
 FT /FTId-VSP\_000465.  
 FT VARSPLIC 487 503 KPLHMPGGDGHGRKSLK -> FCVLRSPSPCLGELTVTEGKA (in isoform 14-AE3).  
 FT /FTId-VSP\_000466.  
 FT VARSPLIC 504 1227 Missing (in isoform 14-AE3).  
 FT /FTId-VSP\_000467.  
 FT SEQUENCE 1227 AA; 135164 MW; D5BEC4E03F4251C CRC64;  
 Query Match 60.7%; Score 68; DB 1; Length 1227;  
 Best Local Similarity 61.1%; Pred. No. 0.021;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 RILLFKPKYHPDPVYV 19  
 Db 1125 RLLLFMPAKHHPEQPYV 1142  
 RESULT 11  
 B3A3\_RAT  
 ID B3A3\_RAT STANDARD; PRT; 1227 AA.  
 AC P23348;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Anion exchange protein 3 (Neuronal band 3-like protein).  
 GN SLC4A3 OR AE3 OR B3RP3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90094439; PubMed=2294114;  
 RA Kudrycki K.E., Newman P.R., Shull G.E.;  
 RT "cDNA cloning and tissue distribution of mRNAs for two proteins that  
 are related to the band 3 Cl-/HCO3-exchanger.";  
 RL J. Biol. Chem. 265:462-471(1990).  
 CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: NEURONAL.  
 CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
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 CC -----  
 DR EMBL; J05167; AAA40798.1; .  
 DR PIR; B34911; B34911.  
 DR HSP; P02730; 1B7Q.  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotranspt.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMS; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 KW Anion exchange; Lipoprotein; Palmitate.  
 FT DOMAIN 1 707 CYTOPLASMIC.  
 FT DOMAIN 708 1227 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 708 730 POTENTIAL.  
 FT TRANSMEM 736 773 POTENTIAL.  
 FT TRANSMEM 793 815 POTENTIAL.  
 FT TRANSMEM 825 846 POTENTIAL.  
 FT TRANSMEM 888 905 POTENTIAL.  
 FT DOMAIN 906 920 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 921 941 POTENTIAL.  
 FT TRANSMEM 975 997 POTENTIAL.  
 FT TRANSMEM 1023 1044 POTENTIAL.  
 FT TRANSMEM 1078 1123 POTENTIAL.  
 FT TRANSMEM 1150 1186 POTENTIAL.  
 FT CARBOHYD 868 868 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 1160 1160 PALMITATE (BY SIMILARITY).  
 FT DOMAIN 74 83 HIS-RICH.  
 FT DOMAIN 135 149 POLY-GLU.  
 FT DOMAIN 155 161 POLY-PRO.  
 FT DOMAIN 307 312 POLY-LYS.  
 FT DOMAIN 441 444 POLY-SER.  
 FT DOMAIN 1179 1182 POLY-LEU.  
 FT SEQUENCE 1227 AA; 135406 MW; 3EB1620BE011730E CRC64;  
 Query Match 60.7%; Score 68; DB 1; Length 1227;  
 Best Local Similarity 61.1%; Pred. No. 0.021;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 RILLFKPKYHPDPVYV 19  
 Db 1125 RLLLFMPAKHHPEQPYV 1142  
 RESULT 12  
 B3A3\_HUMAN  
 ID B3A3\_HUMAN STANDARD; PRT; 1232 AA.  
 AC P48751;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain  
 band 3-like protein) (CAE3/BAE3).  
 GN SLC4A3 OR AE3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM BAE3).  
 RC TISSUE=Heart;  
 RX MEDLINE=95008042; PubMed=7923606;  
 RA Yannoukakis D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,  
 RA Alper S.L.;  
 RT "Molecular cloning, expression, and chromosomal localization of two  
 RT isoforms of the AE3 anion exchanger from human heart.";  
 RL Circ. Res. 75:603-614(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM CAE3).  
 RC TISSUE=Heart;  
 RA Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;

Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
 -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-) EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT CL(-).  
 -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 -!- ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=2;  
 Comment-Additional isoforms seem to exist;  
 Name=BAE3;  
 IsoId=p48751-1; Sequence=Displayed;  
 Name=CAE3;  
 IsoId=p48751-2; Sequence=VSP\_000462, VSP\_000463;  
 -!- TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING VENTRICLE.  
 -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
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 EMBL; U05596; AAA50748.1; -;  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR EMBL; L27213; AAA05850.1; -;  
 DR GO; GO:0005624; C: membrane fraction; TAS.  
 DR PIR; I38496; I38496.  
 DR HSSP; P02730; ILETQ.  
 DR Genew; HGNC:11029; SLC4A3.  
 DR MM; 106195; -;  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO; GO:0005624; C: membrane fraction; TAS.  
 DR GO; GO:0005452; F: inorganic anion exchanger activity; TAS.  
 DR GO; GO:0006832; P: small molecule transport; TAS.  
 DR InterPro; IPR001717; Anion\_exchanger.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3\_cotransp.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 Anion exchange; Lipoprotein; Palmitate; Alternative splicing.  
 FT DOMAIN 1 708 CYTOPLASMIC.  
 FT DOMAIN 709 1232 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 709 731 POTENTIAL.  
 FT TRANSMEM 737 774 POTENTIAL.  
 FT TRANSMEM 794 816 POTENTIAL.  
 FT TRANSMEM 826 847 POTENTIAL.  
 FT TRANSMEM 893 910 POTENTIAL.  
 FT DOMAIN 911 925 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 926 946 POTENTIAL.  
 FT TRANSMEM 980 1002 POTENTIAL.  
 FT TRANSMEM 1028 1049 POTENTIAL.  
 FT TRANSMEM 1083 1128 POTENTIAL.  
 FT TRANSMEM 1155 1191 POTENTIAL.  
 FT DOMAIN 136 149 POLY-GLU.  
 FT DOMAIN 152 161 PRO-RICH.  
 FT DOMAIN 202 207 POLY-SER.  
 FT DOMAIN 308 313 POLY-LYS.  
 FT DOMAIN 442 445 POLY-SER.  
 FT DOMAIN 1184 1187 POLY-LEU.  
 FT LIPID 1165 1165 PALMITATE (BY SIMILARITY).  
 FT VARSPPLIC 1 296 Missing (in isoform CAE3).  
 FT VARSPPLIC 297 299 /FTid=VSP\_000462.  
 FT VARSPPLIC 304 304 SPS -> MPA (in isoform CAE3).  
 FT CONFLICT 304 343 /FTid=VSP\_000463.  
 FT CONFLICT 343 343 I -> V (IN REF. 2).  
 FT CONFLICT 466 466 R -> P (IN REF. 2).  
 FT CONFLICT 608 608 P -> S (IN REF. 2).  
 FT CONFLICT 608 702 S -> G (IN REF. 2).  
 FT CONFLICT 702 702 D -> A (IN REF. 2).

FT CONFLICT 812 813 GS -> FI (IN REF. 2).  
 FT CONFLICT 822 822 F -> L (IN REF. 2).  
 FT CONFLICT 861 861 A -> S (IN REF. 2).  
 FT CONFLICT 863 867 EGSLA -> D (IN REF. 2).  
 FT CONFLICT 875 875 S -> C (IN REF. 2).  
 FT CONFLICT 885 885 S -> G (IN REF. 2).  
 FT CONFLICT 887 887 R -> E (IN REF. 2).  
 FT CONFLICT 899 899 L -> P (IN REF. 2).  
 FT CONFLICT 1096 1096 I -> M (IN REF. 2).  
 SQ SEQUENCE 1232 AA; 135706 MW; 1825BE15977C3821 CRC64;  
 Query Match 55.4%; Score 62; DB 1; Length 1232;  
 Best Local Similarity 55.6%; Pred. No. 0.17;  
 Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 RILLFKPKYKHPDVPYV 19  
 Db 1130 RLLILMPAKHHPEQYV 1147  
 RESULT 13  
 B3A3\_RABIT STANDARD; PRT; 1233 AA.  
 ID B3A3\_RABIT  
 AC O18917;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Anion exchange protein 3 (Neuronal band 3-like protein) (Anion exchanger 3 brain isoform).  
 DE SIC4A3 OR AE3.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Abuladze N., Pushkin A., Kurtz I.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: NEURONAL.  
 CC -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.  
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 CC -----  
 CC EMBL; AF031650; AAB86859.1; -;  
 DR HSSP; P02730; ILETQ.  
 DR InterPro; IPR001717; Anion\_exchanger.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR Pfam; PF00955; HCO3\_cotransp; 1.  
 DR PRINTS; PR01231; HCO3\_cotransp.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 KW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;  
 Anion exchange; Lipoprotein; Palmitate.  
 FT DOMAIN 1 709 CYTOPLASMIC.  
 FT DOMAIN 710 1233 MEMBRANE (ANION EXCHANGE).  
 FT TRANSMEM 710 732 POTENTIAL.  
 FT TRANSMEM 738 775 POTENTIAL.  
 FT TRANSMEM 795 817 POTENTIAL.  
 FT TRANSMEM 827 848 POTENTIAL.  
 FT TRANSMEM 894 911 POTENTIAL.  
 FT DOMAIN 912 926 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 927 947 POTENTIAL.  
 FT TRANSMEM 981 1003 POTENTIAL.

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FT TRANSMEM 1029 1050 POTENTIAL.
FT TRANSMEM 1084 1129 POTENTIAL.
FT TRANSMEM 1156 1192 POTENTIAL.
FT CARBOHYD 874 874 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT LIPID 1166 1166 PALMITATE (BY SIMILARITY).
FT DOMAIN 74 83 HIS-RICH.
FT DOMAIN 136 150 POLY-GLU.
FT DOMAIN 203 208 POLY-SER.
FT DOMAIN 309 312 POLY-LYS.
FT DOMAIN 443 446 POLY-SER.
FT DOMAIN 1185 1198 POLY-LEU.
SQ SEQUENCE 1233 AA; 135759 MW; AE486423E9818583 CRC64;

Query Match
Best Local Similarity 55.4%; Score 62; DB 1; Length 1233;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 RILLLEKPKYHPDVPYV 19
|::: |:::|:::|:::|
DB 1131 RLLILMPAKHHPEQPYV 1148

RESULT 14
SOC7_HUMAN STANDARD; PRT; 440 AA.
AC Q8WXH5;
AT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Suppressor of cytokine signaling 7 (SOCS-7).
GN SOCS4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Hilton D.J., Alexander W.S., Nicola N.A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: SOCS family proteins form part of a classical negative
CC feedback system that regulates cytokine signal transduction.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 1 SOCS box domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF248415; AAL60517.1; -.
CC Genew; HGNC:19392; SOCS7.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001496; SOCS.
CC Pfam; PF00017; SH2; 1.
CC ProDom; PD000093; SH2; 1.
CC SMART; SM00252; SH2; 1.
CC SMART; SM00253; SOCS; 1.
CC PROSITE; PS00001; SH2; 1.
CC PROSITE; PS02225; SOCS; 1.
CC SH2 domain; Growth regulation; Signal transduction inhibitor.
FT DOMAIN 286 381
FT DOMAIN 376 425 SOCS BOX.
SQ SEQUENCE 440 AA; 50623 MW; A4A747AB7F6FF08C CRC64;

Query Match
Best Local Similarity 51.8%; Score 58; DB 1; Length 440;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 DRILLLEKPKYHPDVPYV 19
| | | | | | | | | | |

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DB 253 DEILQLTPPKYHTQIDYV 271

RESULT 15
LEGC_HUMAN STANDARD; PRT; 336 AA.
AC Q96DT0; Q96DS9; Q96PR9; Q9H258; Q9H259; Q9N202;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Galectin-12 (Galectin-related inhibitor of proliferation).
GN LGALS12 OR GRIPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
RA Kishida K., Matsuda M., Kuriyama H., Kihara S., Nakamura T.,
RA Hotta K., Funahashi T., Matsukawa Y., Takahashi M., Nishizawa H.,
RA Tochino Y., Bodkin N.L., Hansen B.C., Matsuzawa Y.;
RT "Galectin-12, an adipose-expressed galectin-like molecule possessing
RT apoptosis-inducing activity."
RL J. Biol. Chem. 276:34089-34097(2001).
[2]
SEQUENCE FROM N.A. (ISOFORMS B; E AND F).
RA TISSUE=Adipose tissue;
RX MEDLINE=21423969; PubMed=11435439;
RA Hotta K., Funahashi T., Matsukawa Y., Takahashi M., Nishizawa H.,
RA Kishida K., Matsuda M., Kuriyama H., Kihara S., Nakamura T.,
RA Tochino Y., Bodkin N.L., Hansen B.C., Matsuzawa Y.;
RT "Cell cycle regulation by galectin-12, a new member of the galectin
RT superfamily."
RL J. Biol. Chem. 276:20252-20260(2001).
CC -!- FUNCTION: Binds lactose.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=A;
CC IsoId=Q96DT0-1; Sequence=Displayed;
CC Name=B; Synonyms=GRIP1a;
CC IsoId=Q96DT0-2; Sequence=VSP_003100;
CC Name=C;
CC IsoId=Q96DT0-3; Sequence=VSP_003102;
CC Name=D;
CC IsoId=Q96DT0-4; Sequence=VSP_003100, VSP_003102;
CC Name=E; Synonyms=1;
CC IsoId=Q96DT0-5; Sequence=VSP_003099;
CC Name=F; Synonyms=2;
CC IsoId=Q96DT0-6; Sequence=VSP_003099, VSP_003101;
CC -!- TISSUE SPECIFICITY: Not widely expressed. Predominantly expressed
CC in adipose tissue.
CC -!- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
CC DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF244974; AAK77328.1; -.
CC EMBL; AF244975; AAK77329.1; -.
CC EMBL; AF244976; AAK77330.1; -.
CC EMBL; AF244977; AAK77331.1; -.
CC EMBL; AF310686; AAG40863.1; -.
CC EMBL; AF310687; AAG40864.1; -.
CC EMBL; AF222695; AAF34677.1; -.
CC Genew; HGNC:15788; LGALS12.
CC MIM; 606096; -.

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DR InterPro; IPR001079; Galectin.  
DR Pfam; PF00337; Gal-bind\_lectin; 1.  
DR SMART; SM00276; GLECT; 1.  
DR PROSITE; PS00309; GALAPTIN; FALSE\_NEG.  
KW Galaptin; Lectin; Repeat; Nuclear protein; Alternative splicing.  
FT DOMAIN 47 183  
FT DOMAIN 194 336  
FT VARSPLIC 1 22  
FT VARSPLIC 1 61  
FT VARSPLIC 74 74  
FT VARSPLIC 200 208  
FT VARSPLIC 336 AA; 37541 MW; F35D0A0CE509E795 CRC64;  
SQ SEQUENCE 336 AA; 37541 MW; F35D0A0CE509E795 CRC64;  
  
Query Match 46.48; Score 52; DB 1; Length 336;  
Best Local Similarity 57.18; Pred. No. 1.4;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
QY 6 LFKPPKYPHPVYV 19  
: || : || |||  
Db 37 ILQPPVHPVYV 50

Search completed: September 3, 2003, 11:46:59  
Job time : 11.25 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 3, 2003, 11:40:18 ; Search time 44.5 Seconds  
(without alignments)  
115.979 Million cell updates/sec

Title: US-10-087-464-1

Perfect score: 104

Sequence: 1 GMPWLSATTVRSVTHANALT 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rdent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	104	100.0	849	11	Q91ZE7	Q91ze7 rattus norv
2	101	97.1	855	6	Q9TUQ0	Q9tuq0 bos taurus
3	101	97.1	930	6	Q9XSW5	Q9xsw5 bos taurus
4	100	96.2	844	13	Q90579	Q90579 gallus gall
5	95	91.3	812	13	Q8JFT9	Q8jft9 brachydanio
6	95	91.3	912	13	Q91452	Q91452 oncorhynch
7	93	89.4	103	11	Q35225	Q35225 cynomys lud
8	93	89.4	466	11	Q991T5	Q991t5 mus musculu
9	93	89.4	622	6	Q9TU75	Q9tu75 sus scrofa
10	93	89.4	1159	4	Q8TAG3	Q8tag3 homo sapien
11	93	89.4	1219	13	Q90710	Q90710 gallus gall
12	93	89.4	1227	4	Q9UEV4	Q9uey4 homo sapien
13	93	89.4	1232	4	Q9UEV5	Q9uey5 homo sapien
14	93	89.4	1241	4	Q99654	Q99654 homo sapien
15	89	89.4	1241	4	Q9UEY6	Q9uey6 homo sapien
16	89	85.6	160	13	P79877	P79877 lampetra ja

17	89	85.6	1030	11	Q9ERP4	Q9erp4 mus musculu
18	89	85.6	1227	11	Q9ERP5	Q9erp5 mus musculu
19	88.5	85.1	124	4	Q9UDJ1	Q9udj1 homo sapien
20	84	80.8	357	4	Q99416	Q99416 homo sapien
21	84	80.8	357	4	Q13717	Q13717 homo sapien
22	72	69.2	467	5	Q95SW2	Q95sw2 drosophila
23	72	69.2	914	5	Q8MRK3	Q8mrk3 drosophila
24	72	69.2	1161	5	Q8IQD4	Q8iqd4 drosophila
25	72	69.2	1201	5	Q8IQD6	Q8iqd6 drosophila
26	72	69.2	1228	5	Q8IOD5	Q8iod5 drosophila
27	72	69.2	1268	5	Q9VT48	Q9vt48 drosophila
28	66	63.5	1044	4	Q95233	Q95233 homo sapien
29	66	63.5	1087	11	Q8CF83	Q8cfs3 mus musculu
30	66	63.5	1088	4	Q9HCQ6	Q9hqc6 homo sapien
31	66	63.5	1088	11	Q9EST0	Q9est0 mus musculu
32	66	63.5	1088	11	Q8C943	Q8c943 mus musculu
33	66	63.5	1089	11	Q9JKV6	Q9jkv6 mus musculu
34	66	63.5	1089	11	Q8JZR6	Q8jzr6 mus musculu
35	66	63.5	1089	11	Q8BY17	Q8by17 mus musculu
36	66	63.5	1130	4	Q94843	Q94843 homo sapien
37	62	59.6	651	11	Q8BWZ4	Q8bwz4 mus musculu
38	62	59.6	1000	4	Q9UIB9	Q9uib9 homo sapien
39	62	59.6	1018	4	O60350	O60350 homo sapien
40	62	59.6	1090	4	Q9HC88	Q9hc88 homo sapien
41	62	59.6	1214	4	Q9Y6M7	Q9y6m7 homo sapien
42	62	59.6	1218	11	Q9R1N3	Q9rln3 rattus norv
43	62	59.6	1241	11	Q9QYD5	Q9qyd5 rattus norv
44	62	59.6	1254	11	Q9R1L1	Q9r1l1 rattus norv
45	61	58.7	1030	5	Q9VM32	Q9vm32 drosophila

#### ALIGNMENTS

#### RESULT 1

Q91ZE7 ID Q91ZE7 PRELIMINARY; PRT; 849 AA.

AC Q91ZE7;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Band 3 anion exchange protein.

OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Colon;

RA ye H., Binder H.J., Rajendran V.M.;

RT "Molecular cloning and characterization of band 3 anion exchange protein (AEL) mRNA from rat colon.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY030082; AAK38733.1;

DR InterPro; IPR001717; Anion\_exchange.

DR InterPro; IPR003020; HCO3\_cotransp.

DR Pfam; PF00955; HCO3\_cotransp; 1.

DR PRINTS; PR01231; HCO3TRNSPORT.

DR TIGRFAMS; TIGR00834; ae; 1.

DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.

DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.

SQ SEQUENCE 849 AA; 94312 MW; E4B200780CB07D3A CRC64;

Query Match Best Local Similarity 100.0%; Score 104; DB 11; Length 849;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GMPWLSATTVRSVTHANALT 20

Db 658 GMPWLSATTVRSVTHANALT 677

#### RESULT 2

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Q9TUQ0
ID Q9TUQ0 PRELIMINARY; PRT; 855 AA.
AC Q9TUQ0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Band 3 protein.
GN BKB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Koshino I., Inaba M., Matsumoto M., Ono K.;
RT "Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated
RT with decreased mutant mRNA possessing dominant negative effect and
RT dominant hereditary spherocytosis in cattle.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF163828; AAD43354.1; -
DR HSSP; P02730; 1BNX.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 855 AA; 95643 MW; 06CD037334F69872 CRC64;

Query Match 97.1%; Score 101; DB 6; Length 855;
Best Local Similarity 95.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSTVTHANALT 20
| | | | | | | | | | | | | | | | | | | | | |
DB 663 GMPWLSATTVRTVTHANALT 682

RESULT 3
Q9XSW5 PRELIMINARY; PRT; 930 AA.
ID Q9XSW5;
AC Q9XSW5;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Band 3 protein.
GN BEB3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Koshino I., Inaba M., Matsumoto M., Ono K.;
RT "Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated
RT with decreased mutant mRNA possessing dominant negative effect and
RT dominant hereditary spherocytosis in cattle.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF163826; AAD43593.1; -
DR HSSP; P02730; 1BNX.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 930 AA; 104374 MW; 4F6AADFEBAF6A3A1 CRC64;

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Query Match 97.1%; Score 101; DB 6; Length 930;
Best Local Similarity 95.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSTVTHANALT 20
| | | | | | | | | | | | | | | | | | | | | |
DB 738 GMPWLSATTVRTVTHANALT 757

RESULT 4
Q90579 PRELIMINARY; PRT; 844 AA.
ID Q90579;
AC Q90579;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Erythroid anion transporter.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=88216609; PubMed=2835670;
RA Cox J.V., Lazarides E.;
RT "Alternative primary structures in the transmembrane domain of the
RT chicken erythroid anion transporter.";
RL Mol. Cell. Biol. 8:1327-1335(1988).
DR EMBL; M19496; AAA48604.1; -
DR HSSP; P02730; 1BTQ.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRNSPORT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 844 AA; 93808 MW; C463F993D5974276 CRC64;

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Query Match 96.2%; Score 100; DB 13; Length 844;
Best Local Similarity 90.0%; Pred. No. 1.6e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSTVTHANALT 20
| | | | | | | | | | | | | | | | | | | | | |
DB 653 GMPWLSATTVRTTTHANALT 672

RESULT 5
Q8JFT9 PRELIMINARY; PRT; 812 AA.
ID Q8JFT9;
AC Q8JFT9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE SI:d2180G5.1 (novel solute carrier protein) (Fragment).
GN SI:D2180G5.1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimberley A.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL604064; CAD43432.2; -
FT NON_TER 1
SQ SEQUENCE 812 AA; 91488 MW; 855A5600C91E3073 CRC64;

Query Match 91.3%; Score 95; DB 13; Length 812;

```



RESULT 11	
Q90710	
ID	Q90710
AC	PRELIMINARY;
DT	Q90710;
DT	01-NOV-1996 (TREMBlrel. 01, Created)
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE	AE2-1 anion exchanger.
GN	AE2.

RESULT 12	
Q9UEY4	
ID	Q9UEY4 PRELIMINARY; PRT; 1227 AA.
AC	Q9UEY4;
DC	01-MAY-2000 (TReMBLrel. 13, Created)
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE	Anion exchanger 2 type b1.
DE	DE
GN	SLC4A2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxId=9606;
[1]	
RN	SEQUENCE FROM N.A.
RP	
RX	MEDLINE=97179202; PubMed=9027488;
RA	Medina J.F., Acin A., Prieto J.;
RT	"Molecular cloning and characterization of the human AE2 anion
RL	exchanger (SLC4A2) gene.";
RL	Genomics 39:74-85(1997).
[2]	
RN	SEQUENCE FROM N.A.
RP	
RX	MEDLINE=20090621;
RA	Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;
RT	"Tissue-specific N-terminal isoforms from overlapping alternate
RL	promoters of the human AE2 anion exchanger gene.";
RL	Biochem. Biophys. Res. Commun. 267:228-235(2000).
DR	EMBL; U76669; AAF19584.2; .
DR	EMBL; U76667; AAF19584.2; JOINED.
DR	EMBL; U76668; AAF19584.2; JOINED.
DR	HSSP; P02730; IBTQ.
DR	InterPro; IPR001717; Anion_exchange.
DR	InterPro; IPR003020; HCO3_cotranspt.
DR	Pfam; PF00955; HCO3_cotransp; 1.
DR	PRINTS; PR01231; HCO3TRNSPORT.
DR	TIGRfams; TIGR00834; ae; 1.
DR	PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR	PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ	SEQUENCE 1227 AA; 135577 MW; 5DA77714C17FB8E7 CRC64;

```
Query Match      89.4%; Score 93; DB 4; Length 1227;
Best Local Similarity 85.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATVRSVTHANALT 20
Db 1036 GLPWLAATVRSVTHANALT 1055
|:||||:| ||||| |||||

RESULT 13
Q9UEY5 PRELIMINARY; PRT; 1232 AA.
AC Q9UEY5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anion exchanger 2 type b2.
GN SLC4A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97179202; PubMed=9027488;
RA Medina J.F., Acin A., Prieto J.;
RT "Molecular cloning and characterization of the human AE2 anion
exchanger (SLC4A2) gene.";
RL Genomics 39:74-85(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20090621;
RA Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;
RT "Tissue-specific N-terminal isoforms from overlapping alternate
promoters of the human AE2 anion exchanger gene.";
RL Biochem. Biophys. Res. Commun. 267:228-235(2000).
DR EMBL; U76669; AAF23240.1; JOINED.
DR EMBL; U76667; AAF23240.1; JOINED.
DR EMBL; U76668; AAF23240.1; JOINED.
DR HSSP; P02730; 1BTQ.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PRO1231; HCO3TRNSPORT.
DR TIGRFAMS; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 1232 AA; 136218 MW; 22688C662907C2D7 CRC64;

Query Match      89.4%; Score 93; DB 4; Length 1232;
Best Local Similarity 85.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATVRSVTHANALT 20
Db 1041 GLPWLAATVRSVTHANALT 1060
|:||||:| ||||| |||||

RESULT 14
Q9UEY5 PRELIMINARY; PRT; 1241 AA.
AC Q9UEY5;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE AE2 anion exchanger.
GN SLC4A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97179202; PubMed=9027488;
RA Medina J.F., Acin A., Prieto J.;
RT "Molecular cloning and characterization of the human AE2 anion
exchanger (SLC4A2) gene.";
RL Genomics 39:74-85(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20090621;
RA Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;
RT "Tissue-specific N-terminal isoforms from overlapping alternate
promoters of the human AE2 anion exchanger gene.";
RL Biochem. Biophys. Res. Commun. 267:228-235(2000).
DR EMBL; U76669; AAF23240.1; JOINED.
DR EMBL; U76667; AAF23240.1; JOINED.
DR EMBL; U76668; AAF23240.1; JOINED.
DR HSSP; P02730; 1BTQ.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PRO1231; HCO3TRNSPORT.
DR TIGRFAMS; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 1232 AA; 136218 MW; 22688C662907C2D7 CRC64;

Query Match      89.4%; Score 93; DB 4; Length 1241;
Best Local Similarity 85.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATVRSVTHANALT 20
Db 1050 GLPWLAATVRSVTHANALT 1069
|:||||:| ||||| |||||

RESULT 15
Q9UEY6 PRELIMINARY; PRT; 1241 AA.
AC Q9UEY6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anion exchanger 2 type a.
GN SLC4A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97179202; PubMed=9027488;
RA Medina J.F., Acin A., Prieto J.;
RT "Molecular cloning and characterization of the human AE2 anion
exchanger (SLC4A2) gene.";
RL Genomics 39:74-85(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20090621;
RA Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;
RT "Tissue-specific N-terminal isoforms from overlapping alternate
promoters of the human AE2 anion exchanger gene.";
RL Biochem. Biophys. Res. Commun. 267:228-235(2000).
DR EMBL; U76669; AAF19583.2; JOINED.
DR EMBL; U76667; AAF19583.2; JOINED.
DR EMBL; U76668; AAF19583.2; JOINED.
DR HSSP; P02730; 1BTQ.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotransp.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PRO1231; HCO3TRNSPORT.
DR TIGRFAMS; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SQ SEQUENCE 1241 AA; 136980 MW; D2FDA72E20D70D64 CRC64;

Query Match      89.4%; Score 93; DB 4; Length 1241;
Best Local Similarity 85.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GMPWLSATVRSVTHANALT 20
Db 1050 GLPWLAATVRSVTHANALT 1069
|:||||:| ||||| |||||
```

Search completed: September 3, 2003, 11:50:01  
Job time : 46.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:40:18 ; Search time 44.5 Seconds  
(without alignments)  
115.979 Million cell updates/sec

Title: US-10-087-464-1

Perfect score: 104  
Sequence: 1 GMPWLSATTVRSVTHANALT 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23.\*

- 1: sp-archaea.\*
- 2: sp-bacteria.\*
- 3: sp-fungi.\*
- 4: sp-human.\*
- 5: sp-invertebrate.\*
- 6: sp-mammal.\*
- 7: sp-mhc.\*
- 8: sp-organelle.\*
- 9: sp-phage.\*
- 10: sp-plant.\*
- 11: sp-rodent.\*
- 12: sp-virus.\*
- 13: sp-vertebrate.\*
- 14: sp-unclassified.\*
- 15: sp-rvirus.\*
- 16: sp-bacteriap.\*
- 17: sp-archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	849	11 Q91ZE7	Q91ze7 rattus norv
2	101	97.1	855	6 Q9TUQ0	Q9tuq0 bos taurus
3	101	97.1	930	6 Q9XSW5	Q9xsw5 bos taurus
4	100	96.2	844	13 Q90579	Q90579 gallus gall
5	95	91.3	812	13 Q8JFT9	Q8jft9 brachydanio
6	95	91.3	912	13 Q91452	Q91452 oncorhynch
7	93	89.4	103	11 Q35225	Q35225 cynomys lud
8	93	89.4	466	11 Q99LT5	Q99lt5 mus musculu
9	93	89.4	622	6 Q9TU75	Q9tu75 sus scrofa
10	93	89.4	1159	4 Q8TAG3	Q8tag3 homo sapien
11	93	89.4	1219	13 Q90710	Q90710 gallus gall
12	93	89.4	1227	4 Q9UEY4	Q9uey4 homo sapien
13	93	89.4	1232	4 Q9UEY5	Q9uey5 homo sapien
14	93	89.4	1241	4 Q99654	Q99654 homo sapien
15	93	89.4	1241	4 Q9UEY6	Q9uey6 homo sapien
16	89	85.6	160	13 P79877	P79877 lampetra ja

17	89	85.6	1030	11 Q9ERP4	Q9erp4 mus musculu
18	89	85.6	1227	11 Q9ERP5	Q9erp5 mus musculu
19	88.5	85.1	124	4 Q9UDJ1	Q9udj1 homo sapien
20	84	80.8	357	4 Q99416	Q99416 homo sapien
21	84	80.8	357	4 Q13717	Q13717 homo sapien
22	72	69.2	467	5 Q95SW2	Q95sw2 drosophila
23	72	69.2	914	5 Q8MRK3	Q8mrk3 drosophila
24	72	69.2	1161	5 Q8IQD4	Q8iqd4 drosophila
25	72	69.2	1201	5 Q8IQD6	Q8iqd6 drosophila
26	72	69.2	1228	5 Q8IQD5	Q8iqd5 drosophila
27	72	69.2	1268	5 Q9VT48	Q9vt48 drosophila
28	66	63.5	1044	4 Q95233	Q95233 homo sapien
29	66	63.5	1087	11 Q8CFS3	Q8cfs3 mus musculu
30	66	63.5	1088	4 Q9HCO6	Q9hcq6 homo sapien
31	66	63.5	1088	11 Q9EST0	Q9est0 mus musculu
32	66	63.5	1088	11 Q8C943	Q8c943 mus musculu
33	66	63.5	1089	11 Q9UKV6	Q9jxv6 mus musculu
34	66	63.5	1089	11 Q8JZR6	Q8jzr6 mus musculu
35	66	63.5	1089	11 Q8BYI7	Q8byi7 mus musculu
36	66	63.5	1130	4 Q94843	Q94843 homo sapien
37	62	59.6	651	11 Q8BWZ4	Q8bwz4 mus musculu
38	62	59.6	1000	4 Q9UIB9	Q9uib9 homo sapien
39	62	59.6	1018	4 Q6O350	Q6o350 homo sapien
40	62	59.6	1090	4 Q9HC88	Q9hc88 homo sapien
41	62	59.6	1214	4 Q9YGM7	Q9ygm7 homo sapien
42	62	59.6	1218	11 Q9R1N3	Q9rln3 rattus norv
43	62	59.6	1241	11 Q9QYD5	Q9qyd5 rattus norv
44	62	59.6	1254	11 Q9R1L1	Q9rll1 rattus norv
45	61	58.7	1030	5 Q9VM32	Q9vm32 drosophila

## ALIGNMENTS

## RESULT 1

Q91ZE7 PRELIMINARY; PRT; 849 AA.  
 ID Q91ZE7  
 AC Q91ZE7;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Band 3 anion exchange protein.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon;  
 RA Ye H., Binder H.J., Rajendran V.M.;  
 RT "Molecular cloning and characterization of band 3 anion exchange  
 protein (AE1) mRNA from rat colon.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY000882; AAK38733.1;  
 DR InterPro; IPR001717; Anion\_exchange.  
 DR InterPro; IPR003020; HCO3\_cotransp.  
 DR Pfam; PF00955; HCO3\_cotransp.1.  
 DR PRINTS; PR01231; HCO3TRNSPORT.  
 DR TIGRFAMs; TIGR00834; ae; 1.  
 DR PROSITE; PS00219; ANION\_EXCHANGER\_1; 1.  
 DR PROSITE; PS00220; ANION\_EXCHANGER\_2; 1.  
 SQ SEQUENCE 849 AA; 94312 MW; E4B200780CB07D3A CRC64;

Query Match 100.0%; Score 104; DB 11; Length 849;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20

DB 658 GMPWLSATTVRSVTHANALT 677

## RESULT 2

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Wed Sep 3 19:34:08 2003

Q9TUQ0	PRELIMINARY;	PRT;	855 AA.
ID	Q9TUQ0		
AC	Q9TUQ0;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	band 3 protein.		
DE	BKB3.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	Koshino I., Inaba M., Matsumoto M., Ono K.;		
RT	"band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated		
RT	with decreased mutant mRNA possessing dominant negative effect and		
RT	dominant hereditary spherocytosis in cattle.;"		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF163828; AAD43354.1; -		
DR	HSP: P02730; IBNX		
DR	InterPro; IPR001717; Anion_exchange.		
DR	InterPro; IPR003020; HCO3_cotranspt.		
DR	Pfam; PF00955; HCO3_cotransp; 1.		
DR	PRINTS; PR01231; HCO3TRNSPORT.		
DR	TIGRFAMS; TIGR00834; ae; 1.		
DR	PROSITE; PS00219; ANION_EXCHANGER_1; 1.		
DR	PROSITE; PS00220; ANION_EXCHANGER_2; 1.		
SQ	SEQUENCE 855 AA; 95643 MW; 06CD037324F69872 CRC64;		
Query Match			
Best Local Similarity 95.0%; Score 101; DB 6; Length 855;			
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	GMPWLSATTVRSVTHANALT	20
bb	663	GMPWLSATTVRVTTHANALT	682

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RESULT 3
Q9XSW5
ID      Q9XSW5 PRELIMINARY; PRT; 930 AA.
AC      Q9XSW5;
DT      01-NOV-1999 (TrEMBLrel. 12, Created)
DT      01-NOV-1999 (TrEMBLrel. 12, last sequence update)
DE      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DR      Band 3 protein.
GN      BEB3.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
RN      NCBI_Taxid=9913;
RX      [1]
RP      SEQUENCE FROM N.A.
RA      TISSUE=Bone marrow;
RC      Koshino I., Inaba M., Matsumoto M., Ono K.;
RT      "band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated
RT      with decreased mutant mRNA possessing dominant negative effect and
RT      dominant hereditary spherocytosis in cattle.";
RL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RD      EMBL; AF163826; AAD43593.1; -.
DR      HSSP; POZ730; IBNX.
DR      InterPro; IPR001717; Anton_exchange.
DR      InterPro; IPR003020; HCO3_cotranspt.
DR      Pfam; PF00955; HCO3_cotransp; 1.
DR      PRINTS; PR01231; HCO3TRANSPORT.
DR      TIGRfams; TIGR00834; ae; 1.
DR      PROSITE; PS00219; ANTON_EXCHANGER_1; 1.
DR      PROSITE; PS00220; ANTON_EXCHANGER_2; 1.
DR      UNICE 930 AA; 104374 MW; 4F6AADFFBEA63A1 CRC64;

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Query Match          97.1%; Score 101; DB 6; Length 930;
Best Local Similarity 95.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 GMPWLSATTVRSVTHANALT 20
DB      738 GMPWLSATTVRVTTHANALT 757
          |||||
RESULT 4
Q90579          PRELIMINARY;          PRT;      844 AA.
ID AC Q90579;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Erythroid anion transporter.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=88216609; PubMed=2835670;
RX Cox J.V., Lazarides E.;
RA "Cox J.V., Lazarides E.;
FT Alternative primary structures in the transmembrane domain of the
RT chicken erythroid anion transporter.";
RL Mol. Cell. Biol. 8:1327-1335(1988).
RL EMBL; M19496; AAA48604.1; -.
RX HSP; P02730; 1BTO.
DR InterPro; IPR001717; Anion_exchange.
DR InterPro; IPR003020; HCO3_cotranspt.
DR Pfam; PF00955; HCO3_cotransp; 1.
DR PRINTS; PR01231; HCO3TRANSPT.
DR TIGRFAMs; TIGR00834; ae; 1.
DR PROSITE; PS00219; ANION_EXCHANGER_1; 1.
DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.
DR SC SEQUENCE 844 AA; 93808 MW; C463F993D5974276 CRC64;

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Query Match          96.2%; Score 100; DB 13; Length 844;
Best Local Similarity 90.0%; Pred. No. 1.6e-07;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMPWLSATTVRSVTHANALT 20
      |||||
Db 653 GMPWLSATTVRTITHANALT 672

RESULT 5
ID Q8JFT9 PRELIMINARY; PRT; 812 AA.
AC Q8JFT9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SI:d218025.1 (novel solute carrier protein) (fragment).
DE SI:D218025.1
OS Brachydanio rerio (Zebrafish) (Danio rerio),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimberley A.;
RL Submitted (DSC-2002) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AL604064; CAD43432.2; -.
FT NON_TER 1
SQ SEQUENCE 812 AA; 855A5600C91E3073 CRC64;

Query Match          91.3%; Score 95; DB 13; Length 812;

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